
WIRE

(TM)

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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sun Aug 8 17:01:38 1999; Maspar time 13516.58 Seconds
Tabular output not generated.
1569.436 Million cell updates/sec

Title: >US-08-287-669-18
Description: (1-7653) from US08287669.seq (10 of 10)
Perfect Score: 7653
N.A. Sequence: 1 AGATCTGAAATAAGGTGATA.....ATTCTGGTCAGCAAGATCT 7653
Comp: TCTAGACTTTATCCACTAT.....TAAGACCAGTCGTTCTAGA

Scoring table: TABLE jmetric
Gap 60

Nmatch STD: Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: emb158
1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
genbank11
17:gb_bal 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Statistics: Mean 10.846; Variance 5.255; scale 2.064

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	7653	100.0	7653	21	CBLCD3A	Caenorhabditis elegans 0.00e+00
2	4164	54.4	39908	21	CEC48D1	Caenorhabditis elegans 0.00e+00
3	3359	43.9	314495	19	CEY67H2	Caenorhabditis elegans 0.00e+00
4	73	1.0	224746	19	CEY56A3	Caenorhabditis elegans 1.25e-33
5	71	0.9	4917	19	AC006766	Caenorhabditis elegans 4.31e-32
6	71	0.9	4917	22	CBL44E3B	Caenorhabditis elegans 4.31e-32
7	72	0.9	38846	19	AC006696	Caenorhabditis elegans 7.36e-33
8	69	0.9	42724	21	CEY53A2	Caenorhabditis elegans 1.46e-30
9	72	0.9	43152	21	CBLF59B1	Caenorhabditis elegans 7.36e-33
10	72	0.9	43152	21	CBLF59B1	Caenorhabditis elegans 7.36e-33
11	72	0.9	48088	22	CBL44E3A	Caenorhabditis elegans 7.36e-33
12	72	0.9	178553	19	AC006891	Caenorhabditis elegans 7.36e-33
13	72	0.9	245805	20	AC006752	Caenorhabditis elegans 7.36e-33

0.9	245805	20	AC006752	Caenorhabditis elegans 7.36e-33
0.9	298195	19	AC006890	Caenorhabditis elegans 7.36e-33
0.9	306131	19	AC006874	Caenorhabditis elegans 7.36e-33
0.9	319857	19	AC006782	Caenorhabditis elegans 7.36e-33
0.8	22886	22	CCLC13F10	Caenorhabditis elegans 8.80e-24
0.8	37881	21	CEK05C4	Caenorhabditis elegans 8.97e-27
0.8	39184	19	CEY12F11	Caenorhabditis elegans 8.97e-27
0.8	40103	21	CCLF20D6	Caenorhabditis elegans 2.66e-22
0.8	41564	21	CCLF22F7	Caenorhabditis elegans 2.66e-22
0.8	42512	21	CCLM03A1	Caenorhabditis elegans 2.66e-22
0.8	125590	21	CEY49E10	Caenorhabditis elegans 1.59e-24
0.8	183422	19	AC006905	Caenorhabditis elegans 2.66e-22
0.8	275138	19	CEY54E5	Caenorhabditis elegans 8.97e-27
0.8	298406	21	CEY5B8A	Caenorhabditis elegans 2.66e-22
0.8	317781	20	AC006906	Caenorhabditis elegans 4.86e-23
0.8	336638	19	CEY75B8	Caenorhabditis elegans 2.66e-22
0.7	11684	21	CCLD10G5	Caenorhabditis elegans 1.20e-18
0.7	11775	22	CCLH22D07	Caenorhabditis elegans 6.31e-18
0.7	12712	21	CEW09E7	Caenorhabditis elegans 6.31e-18
0.7	13610	21	CEK08F9	Caenorhabditis elegans 6.31e-18
0.7	19383	21	CER11H6	Caenorhabditis elegans 3.30e-17
0.7	21095	21	CCLD10G5	Caenorhabditis elegans 6.31e-18
0.7	23793	21	CCLW09C3	Caenorhabditis elegans 7.86e-21
0.7	24709	21	CEC26H9A	Caenorhabditis elegans 1.20e-18
0.7	26894	22	CCLH43I07	Caenorhabditis elegans 1.20e-18
0.7	30911	21	CER06C7	Caenorhabditis elegans 1.45e-21
0.7	32788	21	CEK03H1	Caenorhabditis elegans 6.31e-18
0.7	33883	21	CCLK03E5	Caenorhabditis elegans 6.31e-18
0.7	34356	21	CCLW10C8	Caenorhabditis elegans 6.31e-18
0.7	34852	22	CCLW05F2	Caenorhabditis elegans 2.26e-19
0.7	35654	21	CER05D7	Caenorhabditis elegans 1.20e-18
0.7	35782	21	CCLF49D11	Caenorhabditis elegans 1.20e-18
0.7	36004	21	CCLW08A12	Caenorhabditis elegans 1.71e-16
0.7	36309	21	CEP45G2	Caenorhabditis elegans 1.71e-16
0.7	36404	22	CCLD1037	Caenorhabditis elegans 6.31e-18
0.7	36454	19	AC006670	Caenorhabditis elegans 7.86e-21
0.7	36454	19	AC006670	Caenorhabditis elegans 1.20e-18
0.7	37628	21	CEY31D4	Caenorhabditis elegans 4.23e-20
0.7	37711	21	CEK8K96	Caenorhabditis elegans 1.45e-21
0.7	38112	22	CCLR08C7	Caenorhabditis elegans 2.26e-19
0.7	38419	22	CCLF23C8	Caenorhabditis elegans 1.71e-16
0.7	38523	21	CEY39A1B	Caenorhabditis elegans 7.86e-21
0.7	38843	21	CCLT03F1	Caenorhabditis elegans 2.26e-19
0.7	39565	21	CEK08E3	Caenorhabditis elegans 2.26e-19
0.7	39643	21	CCLC25G6	Caenorhabditis elegans 3.30e-17
0.7	41553	21	CCLF53G12	Caenorhabditis elegans 3.30e-17
0.7	42426	22	CCLC39F7	Caenorhabditis elegans 1.71e-16
0.7	48096	21	CET20G5	Caenorhabditis elegans 7.86e-21
0.7	110000	19	CEY38E10	Caenorhabditis elegans 1.20e-18
0.7	115355	19	CEY55D9	Caenorhabditis elegans 1.20e-18
0.7	129060	21	CEY41C4A	Caenorhabditis elegans 3.30e-17
0.7	130294	19	CEY43F11	Caenorhabditis elegans 3.30e-17
0.7	150963	19	AC006727	Caenorhabditis elegans 1.20e-18
0.7	150963	19	AC006727	Caenorhabditis elegans 7.86e-21
0.7	152184	19	CEY70G10	Caenorhabditis elegans 4.23e-20
0.7	152878	21	CEY18D10A	Caenorhabditis elegans 1.45e-21
0.7	169226	19	AC006913	Caenorhabditis elegans 1.45e-21
0.7	171817	19	CEY95D11	Caenorhabditis elegans 1.20e-18
0.7	188972	20	AC006907	Caenorhabditis elegans 3.30e-17
0.7	200509	20	AC006910	Caenorhabditis elegans 1.71e-16
0.7	207370	19	AC006798	Caenorhabditis elegans 2.26e-19
0.7	232854	19	CEY40H4	Caenorhabditis elegans 3.30e-17
0.7	243820	19	CEY75B12	Caenorhabditis elegans 6.31e-18
0.7	247332	19	CEY18D10	Caenorhabditis elegans 4.23e-20
0.7	24940	19	CEY79H2	Caenorhabditis elegans 3.30e-17
0.7	254877	20	AC006904	Caenorhabditis elegans 3.30e-17
0.7	261002	19	CEY41C4	Caenorhabditis elegans 3.30e-17
0.7	262336	19	AC006786	Caenorhabditis elegans 6.31e-18
0.7	262336	19	AC006786	Caenorhabditis elegans 2.26e-19
0.7	263203	19	AC006709	Caenorhabditis elegans 7.86e-21
0.7	267118	20	AC006889	Caenorhabditis elegans 6.31e-18
0.7	269082	19	CEY76A2	Caenorhabditis elegans 1.71e-16
0.7	270192	19	CEY48C3	Caenorhabditis elegans 2.26e-19

87	53	0.7	274626	19	AC006903	Caenorhabditis elegans	1.20e-18	C	160	47	0.6	254877	20	AC006904	Caenorhabditis elegans	2.26e-14
88	56	0.7	274626	19	AC006903	Caenorhabditis elegans	7.86e-21	C	161	49	0.6	276829	20	AC006741	Caenorhabditis elegans	8.78e-16
89	53	0.7	276829	20	AC006741	Caenorhabditis elegans	7.86e-21	C	162	47	0.6	292390	19	AC006900	Caenorhabditis elegans	2.26e-14
90	56	0.7	286715	19	CEY43F3	Caenorhabditis elegans	7.86e-21	C	163	44	0.6	294136	20	AC006901	Caenorhabditis elegans	2.75e-12
91	51	0.7	292390	19	AC006900	Caenorhabditis elegans	3.30e-17	C	164	47	0.6	296699	19	CEY48A6	Caenorhabditis elegans	2.26e-14
92	53	0.7	297070	19	CEY47H10	Caenorhabditis elegans	1.20e-18	C	165	43	0.6	299202	19	AC006792	Caenorhabditis elegans	1.33e-11
93	52	0.7	297866	19	AC006794	Caenorhabditis elegans	6.31e-18	C	166	48	0.6	299719	19	AC006780	Caenorhabditis elegans	4.48e-15
94	50	0.7	298195	19	AC006890	Caenorhabditis elegans	1.71e-16	C	167	48	0.6	299719	19	AC006780	Caenorhabditis elegans	4.48e-15
95	55	0.7	298960	20	AC006896	Caenorhabditis elegans	4.23e-20	C	168	48	0.6	299919	19	AC006712	Caenorhabditis elegans	4.48e-15
96	56	0.7	299300	20	AC006881	Caenorhabditis elegans	7.86e-21	C	169	47	0.6	312267	19	AC006785	Caenorhabditis elegans	2.26e-14
97	56	0.7	299319	19	AC006712	Caenorhabditis elegans	7.86e-21	C	170	47	0.6	337565	19	CEY47D3	Caenorhabditis elegans	2.26e-14
98	53	0.7	306131	19	AC006874	Caenorhabditis elegans	1.20e-18	C	171	37	0.5	2144	21	CEVC50H2R	Caenorhabditis elegans	1.35e-07
99	51	0.7	312367	19	AC006785	Caenorhabditis elegans	3.30e-17	C	172	40	0.5	6751	21	CELMYOD	Caenorhabditis elegans	1.42e-09
100	53	0.7	315330	19	CEY48E5	Caenorhabditis elegans	1.20e-18	C	173	39	0.5	7035	21	CELCY91A	Caenorhabditis elegans	6.56e-09
101	50	0.7	31781	20	AC006906	Caenorhabditis elegans	1.71e-16	C	174	35	0.5	7878	19	AC006831	Caenorhabditis elegans	2.50e-06
102	53	0.7	319857	19	AC006782	Caenorhabditis elegans	1.20e-18	C	175	37	0.5	9662	19	AC006775	Caenorhabditis elegans	1.35e-07
103	55	0.7	326074	19	CEY44A6	Caenorhabditis elegans	4.23e-20	C	176	36	0.5	10169	22	CELF36N01	Caenorhabditis elegans	5.96e-07
104	55	0.7	340801	19	AC006751	Caenorhabditis elegans	4.23e-20	C	177	39	0.5	10556	22	CELF53E2	Caenorhabditis elegans	6.56e-09
105	51	0.7	340801	19	AC006751	Caenorhabditis elegans	4.23e-20	C	178	35	0.5	12614	22	CELY76B12A	Caenorhabditis elegans	6.56e-06
106	43	0.6	4906	21	CELUNC60X	Caenorhabditis elegans	3.30e-17	C	179	38	0.5	12614	22	CELY76B12A	Caenorhabditis elegans	2.99e-08
107	47	0.6	8460	21	CEY52D3	Caenorhabditis elegans	1.33e-11	C	180	40	0.5	12734	21	CEH16D19	Caenorhabditis elegans	1.42e-09
108	47	0.6	8460	21	CEY52D3	Caenorhabditis elegans	2.26e-14	C	181	39	0.5	12734	21	CEH16D19	Caenorhabditis elegans	6.56e-09
109	43	0.6	10556	22	CELF53E2	Caenorhabditis elegans	1.33e-11	C	182	36	0.5	16820	21	CELK10E9	Caenorhabditis elegans	5.96e-07
110	47	0.6	18146	21	CEY39A1C	Caenorhabditis elegans	2.26e-14	C	183	35	0.5	16820	21	CELK10E9	Caenorhabditis elegans	2.50e-06
111	47	0.6	18655	22	CELY49G5B	Caenorhabditis elegans	2.26e-14	C	184	39	0.5	16938	22	CELT25D3	Caenorhabditis elegans	6.56e-09
112	45	0.6	20303	21	CEY81G3A	Caenorhabditis elegans	5.60e-13	C	185	38	0.5	17849	21	CELR03E12	Caenorhabditis elegans	2.99e-08
113	48	0.6	20960	21	CELF17A9	Caenorhabditis elegans	4.48e-15	C	186	37	0.5	18125	22	CELD2063	Caenorhabditis elegans	1.35e-07
114	48	0.6	23483	19	AC006627	Caenorhabditis elegans	4.48e-15	C	187	37	0.5	18555	22	CELY49G5B	Caenorhabditis elegans	1.35e-07
115	47	0.6	23928	21	CEY43F4A	Caenorhabditis elegans	2.26e-14	C	188	37	0.5	19371	21	CEK10G9	Caenorhabditis elegans	1.35e-07
116	49	0.6	26122	21	CELM02F12	Caenorhabditis elegans	8.78e-16	C	189	37	0.5	19529	19	AC006636	Caenorhabditis elegans	1.35e-07
117	43	0.6	26096	19	CEY09D11	Caenorhabditis elegans	1.33e-11	C	190	38	0.5	19588	21	CEFL18A11	Caenorhabditis elegans	2.99e-08
118	47	0.6	30225	21	CEY29C12	Caenorhabditis elegans	2.26e-14	C	191	41	0.5	19588	21	CEFL18A11	Caenorhabditis elegans	3.03e-10
119	47	0.6	32096	21	CEY29A3	Caenorhabditis elegans	2.26e-14	C	192	36	0.5	19934	21	CEY23G7	Caenorhabditis elegans	5.96e-07
120	47	0.6	32205	21	CEK11D9	Caenorhabditis elegans	2.26e-14	C	193	41	0.5	20019	21	CEY17	Caenorhabditis elegans	3.03e-10
121	49	0.6	32218	21	CELM02D3	Caenorhabditis elegans	8.78e-16	C	194	36	0.5	20836	21	CEY54F11	Caenorhabditis elegans	5.96e-07
122	47	0.6	33238	22	CEY06E6	Caenorhabditis elegans	2.26e-14	C	195	42	0.5	22886	22	CELC13F10	Caenorhabditis elegans	6.39e-11
123	47	0.6	33539	22	CELF54E7	Caenorhabditis elegans	2.26e-14	C	196	35	0.5	23483	19	AC006627	Caenorhabditis elegans	2.60e-06
124	49	0.6	33883	21	CELK03E5	Caenorhabditis elegans	8.78e-16	C	197	36	0.5	23793	21	CELM09C3	Caenorhabditis elegans	5.96e-07
125	45	0.6	33963	21	CELT22F3	Caenorhabditis elegans	5.60e-13	C	198	35	0.5	24709	21	CEC26H9A	Caenorhabditis elegans	2.60e-06
126	44	0.6	34132	21	CELT26C12	Caenorhabditis elegans	2.75e-12	C	199	35	0.5	25371	22	CELY23H5A	Caenorhabditis elegans	2.60e-06
127	47	0.6	34728	21	CELF41H10	Caenorhabditis elegans	2.26e-14	C	200	35	0.5	25371	19	AC006728	Caenorhabditis elegans	2.60e-06
128	45	0.6	34907	21	CELM01B12	Caenorhabditis elegans	5.60e-13	C	201	35	0.5	26894	22	CELY43I07	Caenorhabditis elegans	2.50e-06
129	48	0.6	35169	21	CELM02G9	Caenorhabditis elegans	4.38e-11	C	202	37	0.5	27396	21	CELC54G6	Caenorhabditis elegans	1.35e-07
130	43	0.6	35776	21	CELC44E4	Caenorhabditis elegans	1.33e-11	C	203	35	0.5	27567	21	CELT27C4	Caenorhabditis elegans	2.60e-06
131	43	0.6	35855	21	CELC38C3	Caenorhabditis elegans	1.33e-11	C	204	41	0.5	27748	22	CELY34C03	Caenorhabditis elegans	3.03e-10
132	47	0.6	35989	21	CEK1320	Caenorhabditis elegans	2.26e-14	C	205	37	0.5	27777	21	CEY43D2	Caenorhabditis elegans	1.35e-07
133	43	0.6	36306	21	CEM142	Caenorhabditis elegans	1.33e-11	C	206	37	0.5	27809	21	CEY38H4	Caenorhabditis elegans	1.35e-07
134	45	0.6	36999	21	CELM01B11	Caenorhabditis elegans	5.60e-13	C	207	35	0.5	27809	21	CEY38H4	Caenorhabditis elegans	2.60e-06
135	48	0.6	38643	21	CELT03F1	Caenorhabditis elegans	4.48e-15	C	208	37	0.5	27832	21	CEZK1128	Caenorhabditis elegans	1.35e-07
136	45	0.6	39086	21	CEK07A1	Caenorhabditis elegans	5.60e-13	C	209	35	0.5	28026	22	CELY66H1A	Caenorhabditis elegans	2.99e-08
137	44	0.6	39273	22	CELK08D9	Caenorhabditis elegans	2.75e-12	C	210	38	0.5	28762	21	CEY37G6	Caenorhabditis elegans	2.99e-08
138	44	0.6	39565	21	CEK08E3	Caenorhabditis elegans	2.75e-12	C	211	38	0.5	29096	19	CEY09D11	Caenorhabditis elegans	2.99e-08
139	46	0.6	39784	21	CEC14A4	Caenorhabditis elegans	1.13e-13	C	212	37	0.5	29214	21	CELC50F2	Caenorhabditis elegans	1.35e-07
140	44	0.6	40437	21	CELT10B5	Caenorhabditis elegans	2.75e-12	C	213	40	0.5	29214	21	CELC50F2	Caenorhabditis elegans	1.42e-09
141	47	0.6	41553	21	CELF53G12	Caenorhabditis elegans	2.26e-14	C	214	40	0.5	29363	21	CEY37D6	Caenorhabditis elegans	1.42e-09
142	48	0.6	41645	21	CELC03H5	Caenorhabditis elegans	4.48e-15	C	215	42	0.5	29786	21	CEC55A6	Caenorhabditis elegans	6.39e-11
143	43	0.6	43410	21	CEC01G6	Caenorhabditis elegans	1.33e-11	C	216	37	0.5	30274	21	CEY45H11	Caenorhabditis elegans	1.42e-09
144	45	0.6	44132	22	CEY52C12	Caenorhabditis elegans	5.60e-13	C	217	40	0.5	31244	21	CEY43F4B	Caenorhabditis elegans	1.42e-09
145	48	0.6	78153	21	CEY53C10A	Caenorhabditis elegans	4.48e-15	C	218	38	0.5	31255	21	CEY43H10	Caenorhabditis elegans	2.99e-08
146	44	0.6	110000	19	CEY57A10	Caenorhabditis elegans	2.75e-12	C	219	40	0.5	31950	21	CEC38H2	Caenorhabditis elegans	1.42e-09
147	48	0.6	110000	19	CEY57A10	Caenorhabditis elegans	4.48e-15	C	220	36	0.5	31950	21	CEC38H2	Caenorhabditis elegans	5.96e-07
148	47	0.6	110000	19	CEY57A10	Caenorhabditis elegans	2.26e-14	C	221	37	0.5	32048	21	CELY57C9	Caenorhabditis elegans	1.35e-07
149	45	0.6	112726	19	CEY21F11	Caenorhabditis elegans	5.60e-13	C	222	38	0.5	32205	21	CEK11D9	Caenorhabditis elegans	2.99e-08
150	44	0.6	140702	20	AC006888	Caenorhabditis elegans	2.75e-12	C	223	39	0.5	32215	21	CEW02B9	Caenorhabditis elegans	6.56e-09
151	48	0.6	145920	19	AC006710	Caenorhabditis elegans	4.48e-15	C	224	42	0.5	32218	21	CELR02D3	Caenorhabditis elegans	5.96e-07
152	44	0.6	159453	19	AC006732	Caenorhabditis elegans	2.75e-12	C	225	36	0.5	32556	22	CELT27C10	Caenorhabditis elegans	3.03e-10
153	46	0.6	163125	19	AC006324	Homo sapiens clone DJ1	1.13e-13	C	226	41	0.5	32677	21	CEC08F8	Caenorhabditis elegans	2.60e-06
154	44	0.6	173140	19	AC004867	Homo sapiens clone DJ1	1.13e-13	C	227	35	0.5	32715	21	CEY54F12	Caenorhabditis elegans	1.42e-09
155	43	0.6	201746	20	AC006895	Caenorhabditis elegans	1.33e-11	C	228	40	0.5	32715	21	CEY54F12	Caenorhabditis elegans	2.60e-06
156	48	0.6	201746	20	AC006895	Caenorhabditis elegans	4.48e-15	C	229	35	0.5	32819	19	CEH37L19	Caenorhabditis elegans	6.56e-09
157	49	0.6	206217	19	AC006754	Caenorhabditis elegans	8.78e-16	C	230	39	0.5	33000	21	CEX11H3	Caenorhabditis elegans	1.35e-07
158	46	0.6	207370	19	AC006798	Caenorhabditis elegans	1.13e-13	C	231	37	0.5	33156	21	CEY25E12	Caenorhabditis elegans	6.56e-09
159	47	0.6	242893	19	CEY53C12	Caenorhabditis elegans	2.26e-14	C	232	39	0.5	33238	21	CEY06E6	Caenorhabditis elegans	6.56e-09

c	233	39	0.5	33270	21	CELR02F11	Caenorhabditis elegans	6.56e-09	c	306	35	0.5	42537	19	AC006645	Caenorhabditis elegans	2.60e-06
c	234	36	0.5	33477	21	CELR07C4	Caenorhabditis elegans	5.96e-07	c	307	42	0.5	42703	21	CEC09F9	Caenorhabditis elegans	6.39e-11
c	235	39	0.5	33477	21	CELR07C4	Caenorhabditis elegans	6.56e-09	c	308	35	0.5	42923	21	CELC24H12	Caenorhabditis elegans	2.60e-06
c	236	40	0.5	33511	21	CEK1010	Caenorhabditis elegans	1.42e-09	c	309	35	0.5	42953	21	CELC31F4	Caenorhabditis elegans	2.60e-06
c	237	36	0.5	33520	21	CELR02E1	Caenorhabditis elegans	5.96e-07	c	310	37	0.5	43148	21	CEFS2F12	Caenorhabditis elegans	5.96e-07
c	238	37	0.5	33650	21	CEK01A11	Caenorhabditis elegans	1.35e-07	c	311	37	0.5	43395	21	CEFS6A7A	Caenorhabditis elegans	1.35e-07
c	239	38	0.5	33921	21	CEW09D10	Caenorhabditis elegans	2.99e-08	c	312	36	0.5	43395	21	CEFS6A7A	Caenorhabditis elegans	5.96e-07
c	240	36	0.5	34256	21	CELR10C8	Caenorhabditis elegans	5.96e-07	c	313	37	0.5	43726	21	CELC32B8	Caenorhabditis elegans	1.35e-07
c	241	35	0.5	34350	21	CELF56H1	Caenorhabditis elegans	2.99e-08	c	314	36	0.5	45348	19	AC006624	Caenorhabditis elegans	5.96e-07
c	242	38	0.5	34376	21	CELR23B8	Caenorhabditis elegans	2.99e-08	c	315	39	0.5	48088	22	CELY44E3A	Caenorhabditis elegans	6.56e-09
c	243	41	0.5	34775	22	CELR08F4	Caenorhabditis elegans	3.03e-10	c	316	40	0.5	48173	19	CEY38H8	Caenorhabditis elegans	1.42e-09
c	244	36	0.5	34831	21	CEC47G2	Caenorhabditis elegans	5.96e-07	c	317	40	0.5	48985	19	CEW03G8	Caenorhabditis elegans	1.42e-09
c	245	36	0.5	35077	21	CEY38H8A	Caenorhabditis elegans	5.96e-07	c	318	41	0.5	48985	19	CEW03G8	Caenorhabditis elegans	3.03e-10
c	246	40	0.5	35077	21	CEY38H8A	Caenorhabditis elegans	1.42e-09	c	319	39	0.5	67943	19	AC006722	Caenorhabditis elegans	5.96e-07
c	247	38	0.5	35165	21	CEY38H8A	Caenorhabditis elegans	2.99e-08	c	320	41	0.5	67943	19	AC006722	Caenorhabditis elegans	1.35e-07
c	248	35	0.5	35503	21	CEW09D6	Caenorhabditis elegans	2.60e-06	c	321	37	0.5	75073	21	CEY48A6B	Caenorhabditis elegans	1.35e-07
c	249	38	0.5	35564	21	CELR23B11	Caenorhabditis elegans	2.99e-08	c	322	37	0.5	95182	21	CEY54G11A	Caenorhabditis elegans	1.35e-07
c	250	36	0.5	35854	21	CELR05D7	Caenorhabditis elegans	5.96e-07	c	323	37	0.5	95182	21	CEY54G11A	Caenorhabditis elegans	6.56e-09
c	251	36	0.5	35804	21	CELR10C2	Caenorhabditis elegans	5.96e-07	c	324	39	0.5	95988	21	CEY47D3B	Caenorhabditis elegans	6.56e-09
c	252	42	0.5	35879	21	CEW02A2	Caenorhabditis elegans	6.39e-11	c	325	41	0.5	95988	21	CEY47D3B	Caenorhabditis elegans	3.03e-10
c	253	35	0.5	36004	21	CELR08A12	Caenorhabditis elegans	2.60e-06	c	326	38	0.5	101584	19	AC006793	Caenorhabditis elegans	2.99e-08
c	254	26	0.5	36302	21	CEY48C2	Caenorhabditis elegans	5.96e-07	c	327	40	0.5	110000	19	CEY39E4	Caenorhabditis elegans	1.42e-09
c	255	40	0.5	36306	21	CEY48C2	Caenorhabditis elegans	5.96e-07	c	328	40	0.5	110000	19	CEY39E4	Caenorhabditis elegans	1.42e-09
c	256	35	0.5	36654	21	CEY45F3A	Caenorhabditis elegans	2.60e-06	c	329	39	0.5	110000	19	CEY39A1	Caenorhabditis elegans	6.56e-09
c	257	37	0.5	36780	19	CEH10N23	Caenorhabditis elegans	6.39e-11	c	330	38	0.5	110000	19	CEY39A1	Caenorhabditis elegans	2.99e-08
c	258	37	0.5	37342	21	CELR18G1	Caenorhabditis elegans	1.35e-07	c	331	38	0.5	110000	19	CEY39A1	Caenorhabditis elegans	5.96e-07
c	259	36	0.5	37353	21	CELR12D8	Caenorhabditis elegans	5.96e-07	c	332	36	0.5	110000	19	CEY106G6	Caenorhabditis elegans	5.96e-07
c	260	37	0.5	37545	21	CEY21C9	Caenorhabditis elegans	1.35e-07	c	333	36	0.5	110000	19	CEY106G6	Caenorhabditis elegans	3.03e-10
c	261	42	0.5	37691	21	CEK05C4	Caenorhabditis elegans	6.39e-11	c	334	41	0.5	110000	19	CEY34E2	Caenorhabditis elegans	1.42e-09
c	262	36	0.5	37711	21	CEY45F3A	Caenorhabditis elegans	5.96e-07	c	335	40	0.5	110000	19	CEY34E2	Caenorhabditis elegans	1.42e-09
c	263	36	0.5	37738	21	CEY45F3A	Caenorhabditis elegans	5.96e-07	c	336	39	0.5	110960	21	CEY39A1A	Caenorhabditis elegans	6.56e-09
c	264	36	0.5	37805	22	CELR03G1	Caenorhabditis elegans	5.96e-07	c	337	40	0.5	110960	21	CEY39A1A	Caenorhabditis elegans	1.42e-09
c	265	35	0.5	37805	22	CELR03G1	Caenorhabditis elegans	2.60e-06	c	338	35	0.5	115355	19	CEY55D9	Caenorhabditis elegans	2.60e-06
c	266	40	0.5	37881	21	CELR09B9	Caenorhabditis elegans	1.42e-09	c	339	42	0.5	125590	21	CEY49E10	Caenorhabditis elegans	6.39e-11
c	267	37	0.5	38112	22	CELR08C7	Caenorhabditis elegans	1.35e-07	c	340	41	0.5	132742	21	CEY37D8A	Caenorhabditis elegans	6.39e-11
c	268	40	0.5	38152	21	CELR03B1	Caenorhabditis elegans	1.42e-09	c	341	42	0.5	132742	21	CEY37D8A	Caenorhabditis elegans	3.03e-10
c	269	40	0.5	38152	21	CELR03B1	Caenorhabditis elegans	1.42e-09	c	342	41	0.5	135550	19	AC006721	Caenorhabditis elegans	2.99e-08
c	270	35	0.5	38561	19	AC006604	Caenorhabditis elegans	2.60e-06	c	343	38	0.5	135550	19	AC006721	Caenorhabditis elegans	1.35e-07
c	271	38	0.5	38561	19	AC006604	Caenorhabditis elegans	2.99e-08	c	344	37	0.5	136764	19	CEY24E3	Caenorhabditis elegans	6.56e-09
c	272	37	0.5	38570	21	CELR06A8	Caenorhabditis elegans	1.35e-07	c	345	39	0.5	140702	20	AC006888	Caenorhabditis elegans	1.42e-09
c	273	39	0.5	38801	19	AC006692	Caenorhabditis elegans	6.56e-09	c	346	40	0.5	150641	21	CEY41E3	Caenorhabditis elegans	2.99e-08
c	274	41	0.5	38846	19	AC006696	Caenorhabditis elegans	3.03e-10	c	347	38	0.5	151727	20	AC006894	Caenorhabditis elegans	1.35e-07
c	275	39	0.5	38876	22	CELR119	Caenorhabditis elegans	6.56e-09	c	348	37	0.5	152878	21	CEY18D10A	Caenorhabditis elegans	1.35e-07
c	276	41	0.5	38890	21	CELC14C11	Caenorhabditis elegans	3.03e-10	c	349	42	0.5	152878	21	CEY18D10A	Caenorhabditis elegans	2.99e-08
c	277	40	0.5	38890	21	CELC14C11	Caenorhabditis elegans	1.42e-09	c	350	37	0.5	16214	20	AC006732	Caenorhabditis elegans	3.03e-10
c	278	42	0.5	38980	21	CELR06C1	Caenorhabditis elegans	6.39e-11	c	351	38	0.5	16214	20	AC006732	Caenorhabditis elegans	1.42e-09
c	279	42	0.5	38984	22	CELP56E10	Caenorhabditis elegans	1.42e-09	c	352	41	0.5	178443	19	CEY38F1	Caenorhabditis elegans	5.96e-07
c	280	40	0.5	39184	19	CELR12F11	Caenorhabditis elegans	6.39e-11	c	353	41	0.5	178443	19	CEY38F1	Caenorhabditis elegans	1.35e-07
c	281	42	0.5	39211	21	CEY36F7	Caenorhabditis elegans	5.96e-07	c	354	40	0.5	178553	19	AC006891	Caenorhabditis elegans	1.35e-07
c	282	36	0.5	39235	21	CEY36F7	Caenorhabditis elegans	5.96e-07	c	355	42	0.5	178553	19	AC006891	Caenorhabditis elegans	2.99e-08
c	283	40	0.5	39333	21	CEY0564	Caenorhabditis elegans	2.60e-06	c	356	39	0.5	179854	19	CEY19D2	Caenorhabditis elegans	6.39e-11
c	284	35	0.5	39614	22	CELR0336	Caenorhabditis elegans	2.99e-08	c	357	40	0.5	179854	19	CEY19D2	Caenorhabditis elegans	1.35e-07
c	285	38	0.5	39931	21	CEY36F7	Caenorhabditis elegans	1.42e-09	c	358	40	0.5	185550	19	CEY44F5	Caenorhabditis elegans	2.60e-06
c	286	40	0.5	39941	21	CEY36F7	Caenorhabditis elegans	1.35e-07	c	359	39	0.5	185550	19	CEY44F5	Caenorhabditis elegans	1.42e-09
c	287	37	0.5	39941	21	CEY36F7	Caenorhabditis elegans	1.35e-07	c	360	37	0.5	200509	20	AC006910	Caenorhabditis elegans	6.56e-09
c	288	40	0.5	39973	21	CEM106	Caenorhabditis elegans	1.42e-09	c	361	37	0.5	200509	20	AC006910	Caenorhabditis elegans	1.35e-07
c	289	42	0.5	39973	21	CEM106	Caenorhabditis elegans	6.39e-11	c	362	38	0.5	204594	19	AC006788	Caenorhabditis elegans	5.96e-07
c	290	42	0.5	40437	21	CELR10B5	Caenorhabditis elegans	6.39e-11	c	363	37	0.5	224525	19	CEY70C5	Caenorhabditis elegans	5.96e-07
c	291	41	0.5	40453	21	CELR09H10	Caenorhabditis elegans	3.03e-10	c	364	36	0.5	224525	19	CEY70C5	Caenorhabditis elegans	1.35e-07
c	292	35	0.5	40662	21	CEY32B12B	Caenorhabditis elegans	2.60e-06	c	365	39	0.5	232854	19	CEY40H4	Caenorhabditis elegans	6.56e-09
c	293	39	0.5	40780	21	CEM03C11	Caenorhabditis elegans	5.96e-07	c	366	37	0.5	232854	19	CEY40H4	Caenorhabditis elegans	1.35e-07
c	294	36	0.5	40921	21	CELR0432	Caenorhabditis elegans	2.60e-06	c	367	37	0.5	233941	19	CEY52B11	Caenorhabditis elegans	6.39e-11
c	295	35	0.5	40999	21	CELF56A6	Caenorhabditis elegans	2.60e-06	c	368	42	0.5	247332	19	CEY18D10	Caenorhabditis elegans	1.42e-09
c	296	41	0.5	40999	21	CELF56A6	Caenorhabditis elegans	1.35e-07	c	369	40	0.5	256941	19	CEY62E10	Caenorhabditis elegans	1.42e-09
c	297	37	0.5	41179	21	CELR01D7	Caenorhabditis elegans	1.35e-07	c	370	37	0.5	256941	19	CEY62E10	Caenorhabditis elegans	1.35e-07
c	298	39	0.5	41258	21	CELR08F1	Caenorhabditis elegans	6.56e-09	c	371	40	0.5	257728	19	AC006846	Caenorhabditis elegans	5.96e-07
c	299	39	0.5	41313	21	CELR16C10	Caenorhabditis elegans	6.56e-09	c	372	36	0.5	260699	20	AC006893	Caenorhabditis elegans	1.42e-09
c	300	39	0.5	41316	22	CELR01B4	Caenorhabditis elegans	6.56e-09	c	373	36	0.5	263203	20	AC006709	Caenorhabditis elegans	2.99e-08
c	301	41	0.5	41316	22	CELR01B4	Caenorhabditis elegans	3.03e-10	c	374	38	0.5	267118	20	AC006889	Caenorhabditis elegans	6.56e-09
c	302	35	0.5	41645	21	CELR03H5	Caenorhabditis elegans	2.60e-06	c	375	39	0.5	270192	19	CEY48C3	Caenorhabditis elegans	6.56e-09
c	303	41	0.5	41778	21	CELR04G7	Caenorhabditis elegans	3.03e-10	c	376	42	0.5	274498	19	AC006765	Caenorhabditis elegans	6.39e-11
c	304	40	0.5	42282	21	CELR0304	Caenorhabditis elegans	1.42e-09	c	377	41	0.5	275138	19	CEY54E5	Caenorhabditis elegans	3.03e-10
c	305	42	0.5	42391	21	CEY28F8	Caenorhabditis elegans	6.39e-11	c	378	39	0.5	278007	19	AC006799	Caenorhabditis elegans	6.56e-0

C 379	C 379	0.5	291622	19	AC006796	Caenorhabditis elegans	5.96e-07	452	34	0.4	23113	21	CEL736A8	Caenorhabditis elegans	1.11e-05
C 380	C 380	0.5	291821	19	CEY48E1	Caenorhabditis elegans	1.96e-07	453	32	0.4	23114	21	CEL754D11	Caenorhabditis elegans	1.94e-04
C 381	C 381	0.5	296699	19	CEY48A6	Caenorhabditis elegans	1.35e-07	454	33	0.4	23114	21	CEL754D11	Caenorhabditis elegans	4.70e-05
C 382	C 382	0.5	297070	19	CEY47H10	Caenorhabditis elegans	5.96e-07	455	33	0.4	23536	21	CEL728H1	Caenorhabditis elegans	4.70e-05
C 383	C 383	0.5	297866	19	AC006794	Caenorhabditis elegans	1.42e-09	456	29	0.4	23281	21	CEY43F4A	Caenorhabditis elegans	1.21e-02
C 384	C 384	0.5	298960	20	AC006896	Caenorhabditis elegans	6.56e-09	457	33	0.4	24281	21	CEC06H2	Caenorhabditis elegans	4.70e-05
C 385	C 385	0.5	299202	19	AC006792	Caenorhabditis elegans	2.99e-08	458	30	0.4	23260	21	CEY90	Caenorhabditis elegans	3.12e-03
C 386	C 386	0.5	299308	19	AC006898	Caenorhabditis elegans	2.60e-06	459	28	0.4	23371	22	CEY23H5A	Caenorhabditis elegans	4.59e-02
C 387	C 387	0.5	299308	19	AC006898	Caenorhabditis elegans	3.03e-10	460	28	0.4	23371	19	AC006728	Caenorhabditis elegans	4.59e-02
C 388	C 388	0.5	299719	19	AC006858	Caenorhabditis elegans	2.60e-06	461	32	0.4	23468	21	CEY14F7	Caenorhabditis elegans	1.94e-04
C 389	C 389	0.5	299719	19	AC006858	Caenorhabditis elegans	2.60e-06	462	31	0.4	23500	21	CELT20F5	Caenorhabditis elegans	7.87e-04
C 390	C 390	0.5	299782	19	AC006844	Caenorhabditis elegans	6.39e-11	463	32	0.4	26209	21	CEY33E4A	Caenorhabditis elegans	1.94e-04
C 391	C 391	0.5	309026	19	AC006760	Caenorhabditis elegans	3.03e-10	464	33	0.4	26253	21	CEY70G10A	Caenorhabditis elegans	4.70e-05
C 392	C 392	0.5	309026	19	AC006760	Caenorhabditis elegans	2.99e-08	465	30	0.4	26343	21	CEY45F10A	Caenorhabditis elegans	3.12e-03
C 393	C 393	0.5	314495	19	CEY67H2	Caenorhabditis elegans	6.39e-11	466	27	0.4	27111	21	CEY45F10A	Caenorhabditis elegans	1.70e-01
C 394	C 394	0.5	315330	19	CEY46G5	Caenorhabditis elegans	6.39e-11	467	33	0.4	27178	21	CELT21F3	Caenorhabditis elegans	4.70e-05
C 395	C 395	0.5	335822	19	CEY54G11	Caenorhabditis elegans	1.35e-07	468	29	0.4	27236	21	CEY32F6A	Caenorhabditis elegans	1.70e-01
C 396	C 396	0.5	335822	19	CEY54G11	Caenorhabditis elegans	6.39e-11	469	27	0.4	27236	21	CEY32F6A	Caenorhabditis elegans	1.21e-02
C 397	C 397	0.5	336638	19	CEY75B8	Caenorhabditis elegans	6.39e-11	470	29	0.4	27777	21	CEY32F6A	Caenorhabditis elegans	1.21e-02
C 398	C 398	0.5	337565	19	CEY47D3	Caenorhabditis elegans	6.39e-11	471	29	0.4	27832	21	CEY32F6A	Caenorhabditis elegans	1.21e-02
C 399	C 399	0.4	2229	21	CEPHAL	C.elegans pha-1 mRNA.	1.21e-02	472	29	0.4	28678	21	CELT04D1	Caenorhabditis elegans	1.21e-02
C 400	C 400	0.4	2229	21	CEPHAL	C.elegans pha-1 mRNA.	1.94e-04	473	29	0.4	28678	21	CELT04D1	Caenorhabditis elegans	1.21e-02
C 401	C 401	0.4	5290	20	AC006886	Caenorhabditis elegans	4.59e-02	474	28	0.4	28871	21	CELT04D1	Caenorhabditis elegans	1.21e-02
C 402	C 402	0.4	5535	21	AB000802	Caenorhabditis elegans	3.12e-03	475	28	0.4	29085	21	CEY59C6	Caenorhabditis elegans	4.59e-02
C 403	C 403	0.4	5535	21	AB000802	Caenorhabditis elegans	1.70e-01	476	31	0.4	29283	21	CEY59C6	Caenorhabditis elegans	4.59e-02
C 404	C 404	0.4	7092	21	CEPHALD	C.elegans pha-1 gene.	1.21e-02	477	32	0.4	29283	21	CEY59C6	Caenorhabditis elegans	1.94e-04
C 405	C 405	0.4	7092	21	CEPHALD	C.elegans pha-1 gene.	1.94e-04	478	29	0.4	29303	21	CEY59C6	Caenorhabditis elegans	1.94e-04
C 406	C 406	0.4	7141	21	CELFEM1	C.elegans fem-1 gene.	1.21e-02	479	28	0.4	29303	21	CEY59C6	Caenorhabditis elegans	4.59e-02
C 407	C 407	0.4	7141	21	CELFEM1	C.elegans fem-1 gene.	1.70e-01	480	31	0.4	30098	21	CEY59C6	Caenorhabditis elegans	1.94e-04
C 408	C 408	0.4	7988	21	CELFEM1	C.elegans fem-1 gene.	4.70e-05	481	30	0.4	30522	21	CEY59C6	Caenorhabditis elegans	1.94e-04
C 409	C 409	0.4	9274	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	482	30	0.4	30827	21	CEY59C6	Caenorhabditis elegans	1.70e-01
C 410	C 410	0.4	9314	22	CEY52B11C	Caenorhabditis elegans	4.59e-02	483	31	0.4	30827	21	CEY59C6	Caenorhabditis elegans	1.70e-01
C 411	C 411	0.4	9618	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	484	30	0.4	30911	21	CEY59C6	Caenorhabditis elegans	1.70e-01
C 412	C 412	0.4	9618	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	485	33	0.4	31264	21	CEY59C6	Caenorhabditis elegans	1.70e-01
C 413	C 413	0.4	11684	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	486	33	0.4	31273	21	CEY59C6	Caenorhabditis elegans	1.70e-01
C 414	C 414	0.4	12712	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	487	34	0.4	32209	19	AC006663	Caenorhabditis elegans	1.11e-05
C 415	C 415	0.4	12712	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	488	32	0.4	32209	19	AC006663	Caenorhabditis elegans	1.11e-05
C 416	C 416	0.4	13120	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	489	34	0.4	32263	19	AC0066776	Caenorhabditis elegans	1.11e-05
C 417	C 417	0.4	13610	21	CEY52B11C	Caenorhabditis elegans	4.59e-02	490	30	0.4	32263	19	AC0066776	Caenorhabditis elegans	1.11e-05
C 418	C 418	0.4	13877	21	CEY54E12	Caenorhabditis elegans	4.59e-02	491	31	0.4	32458	21	CEY49E11	Caenorhabditis elegans	1.11e-05
C 419	C 419	0.4	14473	21	CEY54E12	Caenorhabditis elegans	4.59e-02	492	28	0.4	32556	22	CEY49E11	Caenorhabditis elegans	1.11e-05
C 420	C 420	0.4	14473	21	CEY54E12	Caenorhabditis elegans	4.59e-02	493	34	0.4	32556	22	CEY49E11	Caenorhabditis elegans	1.11e-05
C 421	C 421	0.4	14759	21	CEY54E12	Caenorhabditis elegans	4.59e-02	494	33	0.4	32556	22	CEY49E11	Caenorhabditis elegans	1.11e-05
C 422	C 422	0.4	14759	21	CEY54E12	Caenorhabditis elegans	4.59e-02	495	31	0.4	32556	22	CEY49E11	Caenorhabditis elegans	1.11e-05
C 423	C 423	0.4	15704	21	CEY54E12	Caenorhabditis elegans	4.59e-02	496	33	0.4	32556	22	CEY49E11	Caenorhabditis elegans	1.11e-05
C 424	C 424	0.4	16938	22	CEY54E12	Caenorhabditis elegans	4.59e-02	497	27	0.4	32703	21	CEY49E11	Caenorhabditis elegans	1.11e-05
C 425	C 425	0.4	17691	21	CEY57A10	Caenorhabditis elegans	4.59e-02	498	29	0.4	32703	21	CEY49E11	Caenorhabditis elegans	1.11e-05
C 426	C 426	0.4	17716	21	CEY57A10	Caenorhabditis elegans	4.59e-02	499	28	0.4	32880	21	CEY49E11	Caenorhabditis elegans	1.11e-05
C 427	C 427	0.4	17716	21	CEY57A10	Caenorhabditis elegans	4.59e-02	500	27	0.4	32919	19	CEY49E11	Caenorhabditis elegans	1.11e-05
C 428	C 428	0.4	18227	19	CEY57A10	Caenorhabditis elegans	4.59e-02	501	27	0.4	32919	19	CEY49E11	Caenorhabditis elegans	1.11e-05
C 429	C 429	0.4	18351	21	CEY57A10	Caenorhabditis elegans	4.59e-02	502	28	0.4	32919	19	CEY49E11	Caenorhabditis elegans	1.11e-05
C 430	C 430	0.4	18351	21	CEY57A10	Caenorhabditis elegans	4.59e-02	503	34	0.4	32919	19	CEY49E11	Caenorhabditis elegans	1.11e-05
C 431	C 431	0.4	18617	21	CEY57A10	Caenorhabditis elegans	4.59e-02	504	32	0.4	33038	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 432	C 432	0.4	18617	21	CEY57A10	Caenorhabditis elegans	4.59e-02	505	29	0.4	33038	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 433	C 433	0.4	18946	21	CEY57A10	Caenorhabditis elegans	4.59e-02	506	32	0.4	33038	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 434	C 434	0.4	19020	21	CEY57A10	Caenorhabditis elegans	4.59e-02	507	32	0.4	33038	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 435	C 435	0.4	19020	21	CEY57A10	Caenorhabditis elegans	4.59e-02	508	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 436	C 436	0.4	19442	21	CEY57A10	Caenorhabditis elegans	4.59e-02	509	32	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 437	C 437	0.4	19442	21	CEY57A10	Caenorhabditis elegans	4.59e-02	510	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 438	C 438	0.4	19442	21	CEY57A10	Caenorhabditis elegans	4.59e-02	511	28	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 439	C 439	0.4	19442	21	CEY57A10	Caenorhabditis elegans	4.59e-02	512	30	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 440	C 440	0.4	19442	21	CEY57A10	Caenorhabditis elegans	4.59e-02	513	30	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 441	C 441	0.4	19442	21	CEY57A10	Caenorhabditis elegans	4.59e-02	514	30	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 442	C 442	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	515	33	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 443	C 443	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	516	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 444	C 444	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	517	33	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 445	C 445	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	518	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 446	C 446	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	519	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 447	C 447	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	520	29	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 448	C 448	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	521	27	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 449	C 449	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	522	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 450	C 450	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	523	27	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05
C 451	C 451	0.4	20303	19	CEY57A10	Caenorhabditis elegans	4.59e-02	524	31	0.4	33274	21	CEY57A10	Caenorhabditis elegans	1.11e-05

525	c	33	0.4	34511	21	CEL2C404	Caenorhabditis elegans	4.70e-05	598	32	0.4	38990	21	CEP36D3	Caenorhabditis elegans	1.94e-04
526	c	33	0.4	34511	21	CEL2C404	Caenorhabditis elegans	4.70e-05	599	34	0.4	39030	21	CEP41D3	Caenorhabditis elegans	1.11e-05
527	c	27	0.4	34668	21	CET24H10	Caenorhabditis elegans	1.70e-01	600	31	0.4	39121	21	CEP09C6	Caenorhabditis elegans	7.87e-04
528	c	27	0.4	34668	21	CET24H10	Caenorhabditis elegans	1.70e-01	601	34	0.4	39211	21	CEP36F7	Caenorhabditis elegans	1.11e-05
529	c	34	0.4	34700	21	CET44B9	Caenorhabditis elegans	1.11e-05	602	29	0.4	39235	21	CEP32D1	Caenorhabditis elegans	1.21e-02
530	c	30	0.4	34700	21	CET44B9	Caenorhabditis elegans	3.12e-03	603	31	0.4	39271	21	CEP52G2	Caenorhabditis elegans	7.87e-04
531	c	30	0.4	34700	21	CET44B9	Caenorhabditis elegans	7.87e-04	604	32	0.4	39271	21	CEP52G2	Caenorhabditis elegans	1.94e-04
532	c	28	0.4	34775	22	CELW08F4	Caenorhabditis elegans	4.59e-02	605	33	0.4	39273	22	CELW08F4	Caenorhabditis elegans	4.70e-05
533	c	31	0.4	34841	21	CELW08F4	Caenorhabditis elegans	7.87e-04	606	31	0.4	39337	21	CEP32A11	Caenorhabditis elegans	7.87e-04
534	c	32	0.4	34907	21	CELW08F4	Caenorhabditis elegans	1.94e-04	607	34	0.4	39337	21	CEP32A11	Caenorhabditis elegans	1.11e-05
535	c	27	0.4	34928	21	CELW08F4	Caenorhabditis elegans	4.59e-02	608	34	0.4	39356	21	CEP32A11	Caenorhabditis elegans	1.70e-01
536	c	28	0.4	35092	22	CELW08F4	Caenorhabditis elegans	4.59e-02	609	27	0.4	39496	21	CEP32A11	Caenorhabditis elegans	1.94e-04
537	c	33	0.4	35240	21	CELW08F4	Caenorhabditis elegans	7.87e-04	610	32	0.4	39511	21	CEP32A11	Caenorhabditis elegans	1.70e-01
538	c	31	0.4	35417	21	CELW08F4	Caenorhabditis elegans	7.87e-04	611	27	0.4	39750	21	CEP32A11	Caenorhabditis elegans	4.59e-02
539	c	27	0.4	35503	21	CELW08F4	Caenorhabditis elegans	1.70e-01	612	28	0.4	39750	21	CEP32A11	Caenorhabditis elegans	1.11e-05
540	c	27	0.4	35579	22	CELW08F4	Caenorhabditis elegans	1.70e-01	613	34	0.4	39752	22	CELW08F4	Caenorhabditis elegans	1.70e-01
541	c	27	0.4	35686	22	CELW08F4	Caenorhabditis elegans	1.70e-01	614	27	0.4	39752	22	CELW08F4	Caenorhabditis elegans	1.21e-02
542	c	29	0.4	35739	21	CELW08F4	Caenorhabditis elegans	1.21e-02	615	29	0.4	39752	22	CELW08F4	Caenorhabditis elegans	1.70e-01
543	c	32	0.4	35776	21	CELW08F4	Caenorhabditis elegans	1.94e-04	616	27	0.4	39790	21	CEP0019	Caenorhabditis elegans	1.70e-01
544	c	33	0.4	35782	21	CELW08F4	Caenorhabditis elegans	4.70e-05	617	29	0.4	39902	21	CEP0019	Caenorhabditis elegans	1.21e-02
545	c	33	0.4	35850	19	CELW08F4	Caenorhabditis elegans	7.87e-04	618	29	0.4	39902	21	CEP0019	Caenorhabditis elegans	1.70e-01
546	c	31	0.4	35879	21	CELW08F4	Caenorhabditis elegans	7.87e-04	619	27	0.4	39908	21	CEP0019	Caenorhabditis elegans	4.59e-02
547	c	31	0.4	35888	21	CELW08F4	Caenorhabditis elegans	7.87e-04	620	28	0.4	39931	21	CEP0019	Caenorhabditis elegans	1.70e-01
548	c	31	0.4	35985	21	CELW08F4	Caenorhabditis elegans	7.87e-04	621	30	0.4	40090	19	AC006611	Caenorhabditis elegans	3.12e-03
549	c	33	0.4	35985	21	CELW08F4	Caenorhabditis elegans	4.70e-05	622	30	0.4	40265	21	CEP56A8	Caenorhabditis elegans	3.12e-03
550	c	28	0.4	36298	21	CELW08F4	Caenorhabditis elegans	4.59e-02	623	31	0.4	40279	21	CEP56A8	Caenorhabditis elegans	7.87e-04
551	c	28	0.4	36298	21	CELW08F4	Caenorhabditis elegans	4.59e-02	624	33	0.4	40301	21	CEP56A8	Caenorhabditis elegans	4.70e-05
552	c	33	0.4	36298	21	CELW08F4	Caenorhabditis elegans	4.70e-05	625	30	0.4	40457	21	CEP09H10	Caenorhabditis elegans	3.12e-03
553	c	34	0.4	36302	21	CELW08F4	Caenorhabditis elegans	1.11e-05	626	32	0.4	40457	21	CEP09H10	Caenorhabditis elegans	7.87e-04
554	c	31	0.4	36355	21	CELW08F4	Caenorhabditis elegans	7.87e-04	627	32	0.4	40553	21	CEP55C5	Caenorhabditis elegans	1.94e-04
555	c	29	0.4	36355	21	CELW08F4	Caenorhabditis elegans	1.21e-02	628	34	0.4	40553	21	CEP55C5	Caenorhabditis elegans	7.87e-04
556	c	29	0.4	36400	21	CELW08F4	Caenorhabditis elegans	1.70e-01	629	34	0.4	40662	21	CEP55C5	Caenorhabditis elegans	1.11e-05
557	c	33	0.4	36400	21	CELW08F4	Caenorhabditis elegans	4.70e-05	630	30	0.4	40662	21	CEP55C5	Caenorhabditis elegans	3.12e-03
558	c	22	0.4	36490	21	CELW08F4	Caenorhabditis elegans	1.94e-04	631	34	0.4	40780	21	CEM03C11	Caenorhabditis elegans	1.11e-05
559	c	27	0.4	36524	21	CELW08F4	Caenorhabditis elegans	1.70e-01	632	33	0.4	40912	22	CEM03C11	Caenorhabditis elegans	4.70e-05
560	c	32	0.4	36532	21	CELW08F4	Caenorhabditis elegans	1.94e-04	633	34	0.4	40912	22	CEM03C11	Caenorhabditis elegans	1.11e-05
561	c	28	0.4	36749	21	CELW08F4	Caenorhabditis elegans	4.59e-02	634	27	0.4	40921	22	CEM03C11	Caenorhabditis elegans	1.70e-01
562	c	31	0.4	36750	21	CELW08F4	Caenorhabditis elegans	3.12e-03	635	31	0.4	4087	21	CEM03C11	Caenorhabditis elegans	7.87e-04
563	c	30	0.4	36750	21	CELW08F4	Caenorhabditis elegans	1.21e-02	636	31	0.4	4100	21	CEM03C11	Caenorhabditis elegans	1.70e-01
564	c	30	0.4	36780	19	CELW08F4	Caenorhabditis elegans	1.21e-02	637	27	0.4	4100	21	CEM03C11	Caenorhabditis elegans	1.94e-04
565	c	29	0.4	36811	21	CELW08F4	Caenorhabditis elegans	1.21e-02	638	32	0.4	41179	21	CEM03C11	Caenorhabditis elegans	1.94e-04
566	c	28	0.4	36811	21	CELW08F4	Caenorhabditis elegans	1.21e-02	639	32	0.4	41397	21	CEM03C11	Caenorhabditis elegans	7.87e-04
567	c	29	0.4	36879	19	CELW08F4	Caenorhabditis elegans	4.59e-02	640	33	0.4	41564	21	CEM03C11	Caenorhabditis elegans	1.70e-01
568	c	29	0.4	36958	21	CELW08F4	Caenorhabditis elegans	1.21e-02	641	31	0.4	41564	21	CEM03C11	Caenorhabditis elegans	1.70e-01
569	c	34	0.4	36958	21	CELW08F4	Caenorhabditis elegans	1.11e-05	642	27	0.4	41588	21	CEM03C11	Caenorhabditis elegans	1.70e-01
570	c	28	0.4	36999	21	CELW08F4	Caenorhabditis elegans	1.94e-04	643	34	0.4	41754	21	CEM03C11	Caenorhabditis elegans	1.94e-04
571	c	32	0.4	37037	21	CELW08F4	Caenorhabditis elegans	1.94e-04	644	32	0.4	41754	21	CEM03C11	Caenorhabditis elegans	7.87e-04
572	c	34	0.4	37037	21	CELW08F4	Caenorhabditis elegans	1.11e-05	645	31	0.4	42057	21	CEM03C11	Caenorhabditis elegans	7.87e-04
573	c	28	0.4	37329	22	CELW08F4	Caenorhabditis elegans	4.59e-02	646	31	0.4	42126	19	CEM03C11	Caenorhabditis elegans	4.59e-02
574	c	28	0.4	37342	21	CELW08F4	Caenorhabditis elegans	1.11e-05	647	27	0.4	42171	21	CEM03C11	Caenorhabditis elegans	1.70e-01
575	c	34	0.4	37353	21	CELW08F4	Caenorhabditis elegans	1.11e-05	648	28	0.4	42171	21	CEM03C11	Caenorhabditis elegans	1.11e-05
576	c	27	0.4	37527	21	CELW08F4	Caenorhabditis elegans	4.59e-02	649	34	0.4	42391	21	CEM03C11	Caenorhabditis elegans	4.70e-05
577	c	27	0.4	37581	22	CELW08F4	Caenorhabditis elegans	1.70e-01	650	33	0.4	42405	21	CEM03C11	Caenorhabditis elegans	1.94e-04
578	c	33	0.4	37635	21	CELW08F4	Caenorhabditis elegans	4.70e-05	651	32	0.4	42426	22	CEM03C11	Caenorhabditis elegans	4.70e-05
579	c	31	0.4	37635	21	CELW08F4	Caenorhabditis elegans	4.70e-05	652	33	0.4	42472	21	CEM03C11	Caenorhabditis elegans	3.12e-03
580	c	33	0.4	37635	21	CELW08F4	Caenorhabditis elegans	4.70e-05	653	30	0.4	42472	21	CEM03C11	Caenorhabditis elegans	4.70e-05
581	c	33	0.4	37854	21	CELW08F4	Caenorhabditis elegans	1.94e-04	654	33	0.4	42521	21	CEM03C11	Caenorhabditis elegans	1.21e-02
582	c	32	0.4	37892	21	CELW08F4	Caenorhabditis elegans	1.94e-04	655	29	0.4	42521	21	CEM03C11	Caenorhabditis elegans	4.59e-02
583	c	28	0.4	38103	21	CELW08F4	Caenorhabditis elegans	3.12e-03	656	28	0.4	42703	21	CEM03C11	Caenorhabditis elegans	1.11e-05
584	c	30	0.4	38119	22	CELW08F4	Caenorhabditis elegans	4.70e-05	657	34	0.4	42724	21	CEM03C11	Caenorhabditis elegans	1.70e-01
585	c	33	0.4	38119	22	CELW08F4	Caenorhabditis elegans	7.87e-04	658	31	0.4	42995	21	CEM03C11	Caenorhabditis elegans	1.70e-01
586	c	33	0.4	38419	22	CELW08F4	Caenorhabditis elegans	7.87e-04	659	27	0.4	43090	21	CEM03C11	Caenorhabditis elegans	3.12e-03
587	c	34	0.4	38504	21	CELW08F4	Caenorhabditis elegans	1.11e-05	660	30	0.4	43492	21	CEM03C11	Caenorhabditis elegans	1.11e-05
588	c	34	0.4	38523	21	CELW08F4	Caenorhabditis elegans	1.11e-05	661	34	0.4	43726	21	CEM03C11	Caenorhabditis elegans	1.94e-04
589	c	28	0.4	38570	21	CELW08F4	Caenorhabditis elegans	4.59e-02	662	32	0.4	43726	21	CEM03C11	Caenorhabditis elegans	1.94e-04
590	c	34	0.4	38610	21	CELW08F4	Caenorhabditis elegans	1.11e-05	663	30	0.4	44031	19	CEM03C11	Caenorhabditis elegans	3.12e-03
591	c	31	0.4	38681	22	CELW08F4	Caenorhabditis elegans	7.87e-04	664	31	0.4	44090	19	CEM03C11	Caenorhabditis elegans	7.87e-04
592	c	29	0.4	38747	21	CELW08F4	Caenorhabditis elegans	4.59e-02	665	31	0.4	44132	22	CEM03C11	Caenorhabditis elegans	7.87e-04
593	c	28	0.4	38787	21	CELW08F4	Caenorhabditis elegans	3.12e-03	666	27	0.4	45348	19	CEM03C11	Caenorhabditis elegans	1.70e-01
594	c	30	0.4	38862	21	CELW08F4	Caenorhabditis elegans	1.94e-04	667	31	0.4	45438	19	CEM03C11	Caenorhabditis elegans	7.87e-04
595	c	32	0.4	38862	21	CELW08F4	Caenorhabditis elegans	1.94e-04	668	32	0.4	45510	21	CEM03C11	Caenorhabditis elegans	1.94e-04
596	c	30	0.4	38876	22	CELW08F4	Caenorhabditis elegans	3.12e-03	669	28	0.4	45510	21	CEM03C11	Caenorhabditis elegans	4.59e-02
597	c	27	0.4	38984	22	CELW08F4	Caenorhabditis elegans	1.70e-01	670	29	0.4	45713	21	CEM03C11	Caenorhabditis elegans	1.21e-02

c	671	c	671	0.4	47147	21	CELC16A11	Caenorhabditis elegans	1.11e-05	744	32	0.4	293825	19	CEY48B6	Caenorhabditis elegans	1.94e-04
c	672	c	672	0.4	47554	21	CELD1007	Caenorhabditis elegans	4.70e-05	745	33	0.4	293825	19	CEY48B6	Caenorhabditis elegans	1.94e-04
c	673	c	673	0.4	47554	21	CELD1007	Caenorhabditis elegans	1.70e-01	746	33	0.4	294136	20	AC006901	Caenorhabditis elegans	4.70e-05
c	674	c	674	0.4	48270	19	CEY43F4	Caenorhabditis elegans	4.70e-05	747	33	0.4	297900	19	AC006704	Caenorhabditis elegans	4.70e-05
c	675	c	675	0.4	48270	19	CEY43F4	Caenorhabditis elegans	7.87e-04	748	34	0.4	298216	19	AC006875	Caenorhabditis elegans	1.11e-05
c	676	c	676	0.4	48338	19	CEY02D9	Caenorhabditis elegans	1.11e-05	749	32	0.4	298216	19	AC006875	Caenorhabditis elegans	1.11e-05
c	677	c	677	0.4	48338	19	CEY02D9	Caenorhabditis elegans	4.59e-02	750	32	0.4	298406	21	CEY7588A	Caenorhabditis elegans	1.94e-04
c	678	c	678	0.4	59573	21	CEY45F10D	Caenorhabditis elegans	4.59e-02	751	32	0.4	298406	21	CEY7588A	Caenorhabditis elegans	1.94e-04
c	679	c	679	0.4	66004	21	CEY07A9	Caenorhabditis elegans	3.12e-03	752	29	0.4	298804	19	AC006911	Caenorhabditis elegans	1.21e-02
c	680	c	680	0.4	68270	21	CEY7A5A	Caenorhabditis elegans	1.21e-02	753	34	0.4	298804	19	AC006911	Caenorhabditis elegans	1.21e-02
c	681	c	681	0.4	83316	19	CEH16D04	Caenorhabditis elegans	1.21e-02	754	29	0.4	299081	20	AC006892	Caenorhabditis elegans	1.11e-05
c	682	c	682	0.4	89430	19	AC006773	Caenorhabditis elegans	4.59e-02	755	29	0.4	299081	20	AC006892	Caenorhabditis elegans	1.11e-05
c	683	c	683	0.4	75342	21	CEY47H9C	Caenorhabditis elegans	1.11e-05	756	33	0.4	299390	20	AC006714	Caenorhabditis elegans	4.70e-05
c	684	c	684	0.4	82986	19	CEAA2	Caenorhabditis elegans	1.11e-05	757	30	0.4	299390	20	AC006714	Caenorhabditis elegans	4.70e-05
c	685	c	685	0.4	95968	21	CEY113B8	Caenorhabditis elegans	3.12e-03	758	31	0.4	299427	19	AC006914	Caenorhabditis elegans	3.12e-03
c	686	c	686	0.4	103725	20	AC006759	Caenorhabditis elegans	7.87e-04	759	27	0.4	299427	19	AC006914	Caenorhabditis elegans	7.87e-04
c	687	c	687	0.4	104180	19	CEZK340	Caenorhabditis elegans	1.70e-01	760	30	0.4	299670	19	AC006845	Caenorhabditis elegans	1.70e-01
c	688	c	688	0.4	108589	19	AC006795	Caenorhabditis elegans	1.11e-05	761	30	0.4	299670	19	AC006845	Caenorhabditis elegans	1.70e-01
c	689	c	689	0.4	108589	19	AC006795	Caenorhabditis elegans	1.11e-05	762	31	0.4	299727	19	AC006738	Caenorhabditis elegans	3.12e-03
c	690	c	690	0.4	110000	19	CEY37D8	Caenorhabditis elegans	1.11e-05	763	27	0.4	299727	19	AC006738	Caenorhabditis elegans	3.12e-03
c	691	c	691	0.4	110000	19	CEY113B8	Caenorhabditis elegans	4.70e-05	764	31	0.4	300197	19	CEY54G9	Caenorhabditis elegans	7.87e-04
c	692	c	692	0.4	110000	19	CEY45F10	Caenorhabditis elegans	1.94e-04	765	33	0.4	300197	19	CEY54G9	Caenorhabditis elegans	7.87e-04
c	693	c	693	0.4	110000	19	CEY38E10	Caenorhabditis elegans	1.94e-04	766	31	0.4	310173	19	CEY62F5	Caenorhabditis elegans	1.70e-01
c	694	c	694	0.4	110000	19	CEY37D8	Caenorhabditis elegans	1.70e-01	767	34	0.4	310173	19	CEY62F5	Caenorhabditis elegans	1.70e-01
c	695	c	695	0.4	110000	19	CEY45F10	Caenorhabditis elegans	4.70e-05	768	31	0.4	31326	19	AC006802	Caenorhabditis elegans	4.70e-05
c	696	c	696	0.4	110000	19	CEY116A8	Caenorhabditis elegans	1.94e-04	769	34	0.4	31326	19	AC006802	Caenorhabditis elegans	4.70e-05
c	697	c	697	0.4	110000	19	CEY39E4	Caenorhabditis elegans	1.94e-04	770	28	0.4	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05
c	698	c	698	0.4	110000	19	CEY111B2	Caenorhabditis elegans	1.94e-04	771	28	0.4	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05
c	699	c	699	0.4	117864	19	CEY38G4	Caenorhabditis elegans	1.21e-02	772	33	0.3	331326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	700	c	700	0.4	117864	19	CEY38G4	Caenorhabditis elegans	1.21e-02	773	33	0.3	331326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	701	c	701	0.4	119562	19	AC006779	Caenorhabditis elegans	1.11e-05	774	24	0.3	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05
c	702	c	702	0.4	119562	19	AC006779	Caenorhabditis elegans	1.11e-05	775	24	0.3	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05
c	703	c	703	0.4	126356	19	AC006876	Caenorhabditis elegans	3.12e-03	776	24	0.3	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05
c	704	c	704	0.4	126356	19	AC006876	Caenorhabditis elegans	3.12e-03	777	24	0.3	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05
c	705	c	705	0.4	134095	19	AC006915	Caenorhabditis elegans	4.59e-02	778	26	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	706	c	706	0.4	134095	19	AC006915	Caenorhabditis elegans	4.59e-02	779	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	707	c	707	0.4	143062	19	CEY17G7B	Caenorhabditis elegans	1.70e-01	780	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	708	c	708	0.4	143062	19	CEY17G7B	Caenorhabditis elegans	1.70e-01	781	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	709	c	709	0.4	145614	19	AC006804	Caenorhabditis elegans	1.11e-05	782	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	710	c	710	0.4	145614	19	AC006804	Caenorhabditis elegans	1.11e-05	783	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	711	c	711	0.4	145920	19	AC006710	Caenorhabditis elegans	4.70e-05	784	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	712	c	712	0.4	152184	19	CEY70G10	Caenorhabditis elegans	4.70e-05	785	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	713	c	713	0.4	153835	19	CEY6D1	Caenorhabditis elegans	1.70e-01	786	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	714	c	714	0.4	156352	19	CEY26B4	Caenorhabditis elegans	1.70e-01	787	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	715	c	715	0.4	157418	19	AC006912	Caenorhabditis elegans	3.12e-03	788	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	716	c	716	0.4	166214	20	AC006735	Caenorhabditis elegans	4.59e-02	789	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	717	c	717	0.4	171817	19	CEY95D11	Caenorhabditis elegans	1.94e-04	790	26	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	718	c	718	0.4	186306	19	CEY6E2	Caenorhabditis elegans	1.94e-04	791	25	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	719	c	719	0.4	187816	19	CEY32F6	Caenorhabditis elegans	1.21e-02	792	25	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	720	c	720	0.4	188972	20	AC006907	Caenorhabditis elegans	3.12e-03	793	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	721	c	721	0.4	191857	19	CEY32B12	Caenorhabditis elegans	3.12e-03	794	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	722	c	722	0.4	193188	20	AC006884	Caenorhabditis elegans	1.94e-04	795	25	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	723	c	723	0.4	204594	19	AC006788	Caenorhabditis elegans	3.12e-03	796	25	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	724	c	724	0.4	206217	19	AC006754	Caenorhabditis elegans	4.70e-05	797	26	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	725	c	725	0.4	207139	19	CEY17G7	Caenorhabditis elegans	1.11e-05	798	26	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	726	c	726	0.4	209365	19	AC006719	Caenorhabditis elegans	7.87e-04	799	25	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	727	c	727	0.4	224525	19	CEY70C5	Caenorhabditis elegans	1.70e-01	800	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	728	c	728	0.4	227066	19	AC006877	Caenorhabditis elegans	1.21e-02	801	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	729	c	729	0.4	227066	19	AC006877	Caenorhabditis elegans	1.21e-02	802	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	730	c	730	0.4	243820	19	CEY7A5	Caenorhabditis elegans	1.11e-05	803	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	731	c	731	0.4	244239	19	AC006880	Caenorhabditis elegans	7.87e-04	804	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	732	c	732	0.4	244239	19	AC006880	Caenorhabditis elegans	7.87e-04	805	26	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	733	c	733	0.4	24513	19	CEY80D3	Caenorhabditis elegans	1.11e-05	806	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	734	c	734	0.4	24513	19	CEY80D3	Caenorhabditis elegans	1.11e-05	807	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	735	c	735	0.4	249640	19	CEY80D3	Caenorhabditis elegans	1.11e-05	808	26	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	736	c	736	0.4	250178	19	AC006771	Caenorhabditis elegans	4.59e-02	809	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	737	c	737	0.4	250448	19	CEY35E3	Caenorhabditis elegans	1.94e-04	810	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	738	c	738	0.4	260699	20	AC006893	Caenorhabditis elegans	4.70e-05	811	25	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	739	c	739	0.4	261002	19	CEY41C4	Caenorhabditis elegans	1.94e-04	812	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	740	c	740	0.4	265082	19	CEY76A2	Caenorhabditis elegans	1.11e-05	813	24	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	741	c	741	0.4	274498	19	AC006765	Caenorhabditis elegans	4.59e-02	814	23	0.3	341326	19	AC006802	Caenorhabditis elegans	4.59e-02
c	742	c	742	0.4	278007	19	AC006799	Caenorhabditis elegans	1.70e-01	815	23	0.3	341326	19	AC006802	Caenorhabditis elegans	

C	817	23	0.3	26054	21	CELC46A5	Caenorhabditis elegans	2.35e+01	890	25	0.3	36654	21	CEY45F3A	Caenorhabditis elegans	2.13e+00	
C	818	23	0.3	26195	21	CELC04G6	Caenorhabditis elegans	2.35e+01	C	891	25	0.3	36753	21	CELF19F10	Caenorhabditis elegans	2.13e+00
C	819	25	0.3	26283	21	CELF56A3	Caenorhabditis elegans	2.13e+00	C	892	25	0.3	37003	21	CELF33D11	Caenorhabditis elegans	2.13e+00
C	820	26	0.3	26310	21	CELC37A2	Caenorhabditis elegans	6.09e-01	C	893	25	0.3	37310	21	CEZK1098	Caenorhabditis elegans	2.13e+00
C	821	23	0.3	26360	22	CELC07A9	Caenorhabditis elegans	2.35e+01	C	894	23	0.3	37545	21	CET21C9	Caenorhabditis elegans	2.35e+01
C	822	24	0.3	27394	21	CEF32B6	Caenorhabditis elegans	7.19e+00	C	895	26	0.3	37634	22	CELC07D4	Caenorhabditis elegans	6.09e-01
C	823	25	0.3	27396	21	CELC54G6	Caenorhabditis elegans	2.13e+00	C	896	25	0.3	37678	21	CELC08B12	Caenorhabditis elegans	2.13e+00
C	824	25	0.3	27540	21	CELC673	Caenorhabditis elegans	2.13e+00	C	897	24	0.3	37854	21	CEC24H11	Caenorhabditis elegans	2.13e+00
C	825	26	0.3	27567	21	CELC27C4	Caenorhabditis elegans	6.09e-01	C	898	24	0.3	38000	21	CEC36A4	Caenorhabditis elegans	2.13e+00
C	826	23	0.3	27645	21	CELC2K1055	Caenorhabditis elegans	2.35e+01	C	899	25	0.3	38103	21	CEC36A4	Caenorhabditis elegans	2.13e+00
C	827	25	0.3	28026	22	CELF66H1A	Caenorhabditis elegans	2.13e+00	C	900	24	0.3	38463	21	CEK09A1	Caenorhabditis elegans	2.13e+00
C	828	26	0.3	28779	19	AC006824	Caenorhabditis elegans	6.09e-01	C	901	24	0.3	38464	21	CEK08E7	Caenorhabditis elegans	7.19e+00
C	829	24	0.3	28871	21	CELC47B2	Caenorhabditis elegans	7.19e+00	C	902	26	0.3	38464	21	CEK08E7	Caenorhabditis elegans	6.09e-01
C	830	25	0.3	29303	21	CEC13G3	Caenorhabditis elegans	2.13e+00	C	903	25	0.3	38472	21	CER10E8	Caenorhabditis elegans	2.13e+00
C	831	23	0.3	29339	21	CEC13G3	Caenorhabditis elegans	2.13e+00	C	904	23	0.3	38563	21	CET20B3	Caenorhabditis elegans	2.13e+00
C	832	24	0.3	30415	21	CELM03F8	Caenorhabditis elegans	7.19e+00	C	905	24	0.3	38799	21	CEK04D7	Caenorhabditis elegans	2.13e+00
C	833	25	0.3	30500	21	CER10E12	Caenorhabditis elegans	2.13e+00	C	906	24	0.3	39215	21	CEK1054	Caenorhabditis elegans	7.19e+00
C	834	26	0.3	30969	21	CER11B5	Caenorhabditis elegans	6.09e-01	C	907	26	0.3	39339	21	CEK08H10	Caenorhabditis elegans	6.09e-01
C	835	25	0.3	31244	21	CEY43F4B	Caenorhabditis elegans	2.13e+00	C	908	23	0.3	39356	21	CEY32A11	Caenorhabditis elegans	2.35e+01
C	836	23	0.3	31261	21	CELF33G12	Caenorhabditis elegans	2.35e+01	C	909	26	0.3	40124	21	CEY09E8	Caenorhabditis elegans	2.35e+01
C	837	25	0.3	31273	21	CEW05E10	Caenorhabditis elegans	2.13e+00	C	910	24	0.3	40145	21	CEC36A4	Caenorhabditis elegans	6.09e-01
C	838	24	0.3	31306	21	CEY46F3	Caenorhabditis elegans	2.13e+00	C	911	23	0.3	40145	21	CEC36A4	Caenorhabditis elegans	2.13e+00
C	839	26	0.3	31433	21	CELF54C1	Caenorhabditis elegans	6.09e-01	C	912	25	0.3	40202	21	CEC01A2	Caenorhabditis elegans	2.13e+00
C	840	26	0.3	31658	21	CEY48F5	Caenorhabditis elegans	6.09e-01	C	913	23	0.3	40261	21	CELC17G10	Caenorhabditis elegans	2.35e+01
C	841	24	0.3	31737	21	CELC06B9	Caenorhabditis elegans	7.19e+00	C	914	26	0.3	40301	21	CELC1044	Caenorhabditis elegans	6.09e-01
C	842	23	0.3	31843	21	CELF48A11	Caenorhabditis elegans	2.35e+01	C	915	24	0.3	40359	21	CEC01H6	Caenorhabditis elegans	7.19e+00
C	843	23	0.3	31899	22	CELT22H9	Caenorhabditis elegans	2.35e+01	C	916	25	0.3	40392	21	CELCXK1290	Caenorhabditis elegans	2.13e+00
C	844	26	0.3	32009	21	CEW06D8	Caenorhabditis elegans	6.09e-01	C	917	26	0.3	40597	21	CEC25A1	Caenorhabditis elegans	6.09e-01
C	845	24	0.3	32009	21	CEW06D8	Caenorhabditis elegans	7.19e+00	C	918	23	0.3	40767	21	CEC04F12	Caenorhabditis elegans	2.35e+01
C	846	25	0.3	32096	21	CEF21A3	Caenorhabditis elegans	2.13e+00	C	919	24	0.3	41458	21	CERB0454	Caenorhabditis elegans	7.19e+00
C	847	25	0.3	32215	21	CEW02B9	Caenorhabditis elegans	2.13e+00	C	920	24	0.3	41078	22	CELT06A10	Caenorhabditis elegans	7.19e+00
C	848	25	0.3	32243	21	CEY58E10	Caenorhabditis elegans	2.13e+00	C	921	25	0.3	41230	21	CELC14A11	Caenorhabditis elegans	2.13e+00
C	849	24	0.3	32270	21	CEY58E10	Caenorhabditis elegans	7.19e+00	C	922	25	0.3	41255	21	CELF56B6	Caenorhabditis elegans	2.13e+00
C	850	24	0.3	32403	21	CELC03B4	Caenorhabditis elegans	7.19e+00	C	923	25	0.3	41452	21	CER06F6	Caenorhabditis elegans	2.13e+00
C	851	26	0.3	32403	22	CELM04C9	Caenorhabditis elegans	6.09e-01	C	924	24	0.3	41498	21	CERB0454	Caenorhabditis elegans	7.19e+00
C	852	24	0.3	32563	22	CEY54D10	Caenorhabditis elegans	7.19e+00	C	925	25	0.3	42057	21	CELC09H11	Caenorhabditis elegans	2.13e+00
C	853	26	0.3	32566	21	CEY54D10	Caenorhabditis elegans	6.09e-01	C	926	24	0.3	42141	21	CEY54G9A	Caenorhabditis elegans	7.19e+00
C	854	26	0.3	32612	21	CEY94A7B	Caenorhabditis elegans	6.09e-01	C	927	24	0.3	42223	22	CELF53C3	Caenorhabditis elegans	7.19e+00
C	855	24	0.3	32700	21	CEY05D4	Caenorhabditis elegans	7.19e+00	C	928	23	0.3	42528	21	CELB0304	Caenorhabditis elegans	2.35e+01
C	856	25	0.3	32703	21	CEY14D1	Caenorhabditis elegans	2.13e+00	C	929	24	0.3	42528	21	CELB0361	Caenorhabditis elegans	7.19e+00
C	857	23	0.3	32703	21	CELT12F5	Caenorhabditis elegans	2.13e+00	C	930	26	0.3	42812	21	CEY52B11	Caenorhabditis elegans	6.09e-01
C	858	25	0.3	32703	21	CEMT12F5	Caenorhabditis elegans	2.13e+00	C	931	26	0.3	42912	21	CELM03A1	Caenorhabditis elegans	7.19e+00
C	859	25	0.3	32723	21	CEM88	Caenorhabditis elegans	2.13e+00	C	932	24	0.3	43148	21	CEY52F12	Caenorhabditis elegans	7.19e+00
C	860	25	0.3	32729	21	CELC05C8	Caenorhabditis elegans	2.13e+00	C	933	26	0.3	43526	21	CELC10H11	Caenorhabditis elegans	6.09e-01
C	861	24	0.3	32750	21	CELC2K484	Caenorhabditis elegans	7.19e+00	C	934	25	0.3	43526	21	CELC10H11	Caenorhabditis elegans	2.13e+00
C	862	26	0.3	32784	21	CEY08G5	Caenorhabditis elegans	6.09e-01	C	935	24	0.3	43599	21	CELC54D2	Caenorhabditis elegans	7.19e+00
C	863	26	0.3	32838	21	CELC08F11	Caenorhabditis elegans	6.09e-01	C	936	24	0.3	43788	21	CELC10C6	Caenorhabditis elegans	2.35e+01
C	864	23	0.3	32880	21	CEY40F12	Caenorhabditis elegans	2.35e+01	C	937	23	0.3	44090	19	AC006784	Caenorhabditis elegans	2.35e+01
C	865	25	0.3	33089	21	CEC52E2A	Caenorhabditis elegans	2.13e+00	C	938	23	0.3	44371	21	CEC47E8	Caenorhabditis elegans	2.35e+01
C	866	24	0.3	33089	21	CELT05C3	Caenorhabditis elegans	7.19e+00	C	939	26	0.3	44451	21	CELC06E7	Caenorhabditis elegans	6.09e-01
C	867	26	0.3	33103	21	CEY31C3	Caenorhabditis elegans	7.19e+00	C	940	26	0.3	44986	21	CELC42C1	Caenorhabditis elegans	6.09e-01
C	868	26	0.3	33164	21	CEY35C5	Caenorhabditis elegans	6.09e-01	C	941	24	0.3	44986	21	CEC36B1	Caenorhabditis elegans	7.19e+00
C	869	26	0.3	33270	21	CELC02F11	Caenorhabditis elegans	6.09e-01	C	942	23	0.3	45612	21	CELC35E7	Caenorhabditis elegans	2.35e+01
C	870	25	0.3	33330	22	CELF37C12	Caenorhabditis elegans	2.13e+00	C	943	24	0.3	47384	21	CELF22E5	Caenorhabditis elegans	7.19e+00
C	871	26	0.3	33406	21	CEY53C12B	Caenorhabditis elegans	6.09e-01	C	944	23	0.3	48173	19	CEY38H8	Caenorhabditis elegans	2.35e+01
C	872	24	0.3	33478	21	CEY53B2	Caenorhabditis elegans	7.19e+00	C	945	26	0.3	66004	19	CEC07A9	Caenorhabditis elegans	7.19e+00
C	873	25	0.3	33551	21	CELF44E2	C. elegans cosmid F44E	2.13e+00	C	946	26	0.3	70594	19	AC006708	Caenorhabditis elegans	6.09e-01
C	874	26	0.3	34268	21	CELM02D7	Caenorhabditis elegans	6.09e-01	C	947	26	0.3	75073	21	CEY48A6B	Caenorhabditis elegans	6.09e-01
C	875	25	0.3	34766	21	CELC03F8	Caenorhabditis elegans	2.13e+00	C	948	24	0.3	78153	21	CEY53C10A	Caenorhabditis elegans	7.19e+00
C	876	24	0.3	34928	21	CELM01A11	Caenorhabditis elegans	7.19e+00	C	949	23	0.3	82986	19	CEA2	Caenorhabditis elegans	2.35e+01
C	877	25	0.3	35121	21	CEY10G8	Caenorhabditis elegans	7.19e+00	C	950	24	0.3	84704	19	CEY48E1B	Caenorhabditis elegans	7.19e+00
C	878	25	0.3	35220	21	CEY04D3	Caenorhabditis elegans	2.13e+00	C	951	25	0.3	104180	19	CEZK340	Caenorhabditis elegans	2.13e+00
C	879	25	0.3	35686	22	CELF46E10	Caenorhabditis elegans	2.13e+00	C	952	24	0.3	106179	19	HSY90B6	Human DNA sequence ***	7.19e+00
C	880	23	0.3	35770	21	CEDH11	Caenorhabditis elegans	2.35e+01	C	953	25	0.3	110000	19	CEY53C10	Caenorhabditis elegans	2.13e+00
C	881	23	0.3	35855	21	CELC38C3	Caenorhabditis elegans	6.09e-01	C	954	25	0.3	110000	19	CEY105F8	Caenorhabditis elegans	7.19e+00
C	882	26	0.3	35888	21	CEY19B10	Caenorhabditis elegans	6.09e-01	C	955	24	0.3	110000	19	CEY102A5	Caenorhabditis elegans	6.09e-01
C	883	26	0.3	35974	21	CELC28F1	Caenorhabditis elegans	6.09e-01	C	956	24	0.3	110000	19	CEY102A5	Caenorhabditis elegans	6.09e-01
C	884	24	0.3	35974	21	CELC28F1	Caenorhabditis elegans	7.19e+00	C	957	23	0.3	110000	19	CEY102A5	Caenorhabditis elegans	6.09e-01
C	885	24	0.3	36080	21	CER10D12	Caenorhabditis elegans	2.13e+00	C	958	26	0.3	110000	19	CEY105P8	Caenorhabditis elegans	7.19e+00
C	886	23	0.3	36120	21	CEY56D1	Caenorhabditis elegans	7.19e+00	C	959	26	0.3	110000	19	CEY53H1	Caenorhabditis elegans	2.13e+00
C	887	24	0.3	36150	21	CEY27D4	Caenorhabditis elegans	2.13e+00	C	960	25	0.3	110000	19	CEY113B8	Caenorhabditis elegans	7.19e+00
C	888	25	0.3	36170	21	CER10E4	Caenorhabditis elegans	2.13e+00	C	961	24	0.3	110000	19	CEY113B8	Caenorhabditis elegans	7.19e+00
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ACCESSION	Z81049		

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 Cp 1757 CGAAATTTTGTAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTT 1698
 Db 11658 TCGTGCAGAGACCCATTTGAAATTAATCC - GTGCGCTTTTAAAGAGGAATGCCAAATCT 11716
 Cp 1697 TCGTGCAGAGACCCATTTGAAATTAATCCGTGTCGCCCTTTAAAGTGAATGCCAAATCT 1638
 Db 11717 TGTGAAATTTTACGGAACACAAAATTCAGAGAATGCGTATTTAGCATCATATTTGGCG 11776
 Cp 1637 TGTGAAATTTTACGGAACACAAAATTCAGAGAATGCGTATTTAGCATCATATTTGGCG 1579
 Db 11777 CGCAAAATATCTCGTAGCTAGAACTACAGTAATCTTTAAATGACTACCGTAGCGTTGT 11836
 Cp 1578 CGCAAAATATCTCGTAGCTAGAACTACAGTAATCTTTAAATGACTACCGTAGCG - TTGT 1520
 Db 11837 GACGATTTACGGTTTGTCAAAATTCGAAATTTCAAAATTTCAAAATTTGAGCCGTA 11896
 Cp 1519 GACGATTTACGGTTTGTCAAAATTCGAAATTTCAAAATTTCAAAATTTGAGCCGTA 1460
 Db 11897 AATCAGACACAGCGCTACAGTAGTCATTTAAAGAAATTTACTGTAGTTTCGCTACGAGATA 11956
 Cp 1459 AATCAGACACAGCGCTACAGTAGTCATTTAAAGAAATTTACTGTAGTTTCGCTACGAGATA 1400
 Db 11957 TTTTGGCGTCAAAATATTTGCGGAGTACGCAATCTCAGAAATTTGATTTCCCTTAATC 12016
 Cp 1399 TTTTGC - CGTCAAAATATCTGCGGAGTACGCAATCTCAGAAATTTGATTTCCCTTAATC 1341
 Db 12017 GATATGTCGAGCGATTTAAAG - A - CTTT - ACCATTTTGTGAGTTTTCGTTGCTATT 12073
 Cp 1340 GATATGTCGAGCGATTTAAAGAGGAGCTTTTACCAATTTTAGTAGTTTTCGTTGCTATT 1281
 Db 12074 ATGATAATTTTACGATAAATTAATCTCAAAATTCGAAATTTTACGCGGAATATTATAA 12133
 Cp 1280 ATGATAATTTTACGATAAATTAATCTCAAAATTCGAAATTTTACGCGGAATATTATAA 1221
 Db 12134 AATAAGATTTTACGACAGAGAAAGTGTGCGAAGAAATCATAAATTTGAGAGAT 12193
 Cp 1220 AATAAGATTTTACGACAGAGAAAGTGTGCGAAGAAATCATAAATTTGAGAGAT 1161
 Db 12194 ATTCCTTATGATTTGATATTTGCGTAACAAATTTGAGAGAAATTTTGGCGGTTTATTG 12253
 Cp 1160 ATTCCTTATGATTTGATATTTGCGTAACAAATTTGAGAGAAATTTTGGCGGTTTATTG 1101
 Db 12254 CAAATTTTCGCGGAAAAATTTTATGATGCTCGTAAGCATGCGCATGAGAAAAA 12313
 Cp 1100 CAAATTTTCGCGGAAAAATTTTATGATGCTCGTAAGCATGCGCATGAGAAAAA 1041
 Db 12314 GTGATTTGTAGCAGCAATATGAGTCACCCATCTGGACAGTTTCACATTTCTTAAACGAT 12373
 Cp 1040 GTGATTTGTAGCAGCAATATGAGTCACCCATCTGGACAGTTTCACATTTCTTAAACGAT 981
 Db 12374 AATTGACAGGAG - CAGGTGCGCATCGGAGAGTGTACCGGAAACAAACCGGGACAAG 12432
 Cp 980 AATTGACAGGAGAGTGTGCGCATCGGAGAGTGTACCGGAAACAAACCGGGACAAG 921
 Db 12433 TTGAGTATCAAGGACGACGAGAAATGATGAAATGTTGTTACAAATGAAACCGGCGTT 12492
 Cp 920 TTGAGTATCAAGGACGACGAGAAATGATGAAATGTTGTTACAAATGAAACCGGCGTT 861

Db 12493 TACCTGAAAGCTCCTGATCTCATCTAAGATTCCAACCCGCTCATTTGCCCTCCATGCACA 12552
 Cp 860 TACCTGAAAGCTCCTGATCTCATCTAAGATTCCAACCCGCTCATTTGCCCTCCATGCACA 801
 Db 12553 AATATAATGCGATTTGGATTTTAAAGCAATGAAATTTGCACAAAGAGCTATAAATCG 12612
 Cp 800 AATATAATGCGATTTGGATTTTAAAGCAATGAAATTTGCACAAAGAGCTATAAATCG 741
 Db 12613 AAAAGAGCATACCAATAGATACACACTGCTTTCTAAGTGGGTTTCGAAAGAACCCGC 12672
 Cp 740 AAAAGAGCATACCAATAGATACACACTGCTTTCTAAGTGGGTTTCGAAAGAACCCGC 681
 Db 12673 CAAAGAGGTGATGGAGTGGTGGGCTAAGGAAGAGTGCAGAGAGGTCAACATGTTG 12732
 Cp 680 CAAAGAGGTGATGGAGTGGTGGGCTAAGGAAGAGTGCAGAGAGGTCAACATGTTG 621
 Db 12733 AATCTTAGGATTTGTTTGTGTTTACATTAATTTGCCCTCGTAAATTTATTTTGGATTG 12792
 Cp 620 AATCTTAGGATTTGTTTGTGTTTACATTAATTTGCCCTCGTAAATTTATTTTGGATTG 561
 Db 12793 AGTATCGAAATCTATGAGCCATGAACACGAGCGGTGAGGTAAAGGTAAAGGTTTAAAA 12852
 Cp 560 AGTATCGAAATCTATGAGCCATGAACACGAGCGGTGAGGTAAAGGTTTAAAA 501
 Db 12853 GTAGTTTATTAGTAACATAATCGTTTTCACATAAACAGTGGTTTTTAAACGAAACA 12912
 Cp 500 GTAGTTTATTAGTAACATAATCGTTTTCACATAAACAGTGGTTTTTAAACGAAACA 441
 Db 12913 ATGCAAAACCAAGGTTAAATTTATAAATCGATTCGAGAAATCTCAGAAATCTTCTGG 12972
 Cp 440 ATGCAAAACCAAGGTTAAATTTATAAATCGATTCGAGAAATCTCAGAAATCTTCTGG 381
 Db 12973 CAACATAAATCGGAGCGCTTTCTTCAATGATGTAATTAATTCCTTAGCAACAGTTC 13032
 Cp 380 CAACATAAATCGGAGCGCTTTCTTCAATGATGTAATTAATTCCTTAGCAACAGTTC 321
 Db 13033 ACACAAAGAACAAAGAAAAACGACAAAGATGACTGCAAGATAACGAAAAAGGAG 13090
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3
 RESULT CEV67H2 314495 bp DNA HTG 04-MAR-1999
 LOCUS Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from
 DEFINITION clone Y67H2, WORKING DRAFT SEQUENCE.
 ACCESSION AL022475
 NID 94469034
 VERSION AL022475.3 GI:4469034
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 314495)
 AUTHORS McMurray, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-1999) Nematode Sequencing Project, Sanger Centre,
 Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,
 Washington University, St. Louis, MO 63110, USA. E-mail:
 jes@sanger.ac.uk or rw@nematode.wustl.edu
 COMMENT On Mar 22, 1999 this sequence version replaced gi:4468145.
 IMPORTANT: This sequence is unfinished and does not necessarily
 represent the correct sequence. Work on the sequence is in progress
 and the release of this data is based on the understanding that the
 sequence may change as work continues. The sequence may be
 contaminated with foreign sequence from E.coli, yeast, vector,
 phage etc. Order of segments is not known; 800 n's separate
 segments.
 * NOTE: This is a 'working draft' sequence.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES

Location/Qualifiers

Cp	5623	TGTGATAGAAATCACAGGATATCGCAGAATCTCCGTGTGATTCGTGTTTGGCAAGTCTCGA	5564
Db	237454	ATTGTCAGAGCATTCCTCGGAAATTAATAATACAGTTTACATTTAGGAACAAGCGCTGGAA	237513
Cp	5563	ATTGTCAGAGCATTCCTCGGAAATTAATAATACAGTTTACATTTAGGAACAAGCGTGGAA	5504
Db	237514	ATTTTTT- GGGTTTCTTTT- GGTATTTGACGAAAAATGATTTTTT- GGTTTTTGGGAC	237570
Cp	5503	ATTTTTTGGGTTTCTTTTGGTATTTTGCAGAAAA- TTGATTTTTTGGTTTTTGGGAC	5445
Db	237571	CAAAAAACAAAAAATAATCGAATTCGACTTTTTTTTTTGGATTTTTTGGCTTTTTTCGAA	237630
Cp	5444	CAAAAAACAAAAAATAATCGAATTCGACTTTTTTTTTTGGATTTTTTGGCTTTTTTCGAA	5385
Db	237631	GATTTCAATTTACTTTTTTGGTGTATTAGGAAGTTTATTGTCGAATGGTGCAATTTTTGCG	237690
Cp	5384	GATTTCAATTTACTTTTTTGGTGTATTAGGAAGTTTATTGTCGAATGGTGCAATTTTTGCG	5325
Db	237691	GACAAAAACTACGGTACCTGGTCTCGACACGACAAATTTTTTGGTC- AATGCAATGGGT	237749
Cp	5324	GACAAAAACTACGGTACCTGGTCTCGACACGACAAATTTTTTGGTCCCAATGCAATGGGT	5265
Db	237750	GTGCGCCTTTAAGCAGTACTGTAATTTCAAACTCTCGTGTGCTGGATATTTTAAATC	237809
Cp	5264	GTGCGCCTTTAAGCAGTACTGTAATTTCAAACTCTCGAAGCTGGGATATTTTAAATC	5205
Db	237810	GATTTTTCAATCTCTTTTTCTCGATTTGTTTAAAAAAATGTGGGAAAAATCTAGAAAA	237869
Cp	5204	GATTTTTCAATCTCTTTTTCTCGATTTGTTTAAAAAAATTTTG- -AAAAATCTAGAAAA	5147
Db	237870	ATGTTATAAAACTTTTCTAAATCTCTCATGATTTTTTCAAAATTTTGCAAAAATAAACAA	237929
Cp	5146	ATGTTATAAAACTTTTCTAAATCTCTCATGATTTTTTCAATTTTGCAAAAATAAACAA	5087
Db	237930	TCGGATGAATAACTTTTGAATTTGAAATGTGACGTGTTTTGATTTTTATTTGCTTTCCG	237989
Cp	5086	TCGGATGAATAACTTTTGAATTTGAAATGTGACGTGTTTTGATTTTTATTTGCTTTCCG	5027
Db	237990	GAGTGGTTTTTAAAGTTTTTAAAAATACATTTTCATATTGAACACCGTTTCCCAATTTTC	238049
Cp	5026	GAGTGGTTTTTAAAGTTTTTAAAAATACATTTTCATATTGAACACCGTTTCCCAATTTTC	4967
Db	238050	ACAAATTTAAATTTGTCATTTTGGATAATTTGAAATTCAGAAAAATGATTTCTGTGC	238109
Cp	4966	ACAAATTTAAATTTGTCATTTTGGATAATTTGAAATTTGAAAAATTCAGAAAAATGATTTCTGTGC	4907
Db	238110	TATCAAGTTTTGTTATGCGGAAAATTTGCTGAAAATTTACAAACGGTTTTTTTACATCAAT	238169
Cp	4906	TATCAAGTTTTGTTATGCGGAAAATTTGCTGAAAATTTACAAACGGTTTTTTTACATCAAT	4847
Db	238170	ATTATAGAAAAACTTAAGAAAAACACATATATGTAGCGGAAAAAACGAAAAATTTCGAAAC	238229
Cp	4846	ATTATAGAAAAACTTAAGAAAAACACATATATGTAGCGGAAAAAACGAAAAATTTCGAAAC	4787
Db	238230	TAGGTAAATCATTTTCGCGGAAGTTTCAAAATTTTGGTTTTTTCGAAAAATACATTTTG	238289
Cp	4786	TAGGTAAATCATTTTCGCGGAAGTTTCAAAATTTTGGTTTTTTCGAAAAATACATTTTG	4727
Db	238290	CATTTAACAAAAATGTGCTGAGACGGCGCCACATTTTTCGCGCAAAAATGCGAA	238349
Cp	4726	CATTTAACAAAAATGTGCTGAGACGGCGCCACATTTTTCGCGCAAAA- TGSCAA	4668
Db	238350	AAATTTTCGGTTTTGGGTAATAATTTTCGCGGTACCCCTCCCGTCAGATGTCTTTCGAA	238409
Cp	4667	A- -TTTCGGTTTTGGGTAATAATAATTTTCGCGGTACCCCTCCCGTCAGATGTCTTTCGAA	4610
Db	238410	ATAACGTTATGCCCATGCACTGAACAAAATGCTAGATGTGCTTGTGCGCCTTGCTA	238469
Cp	4609	ATAACGTTATGCCCATGCACTGAACAAAATGCTAGATGTGCTTGTGCGCCTTGCTA	4550
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4	CEY56A3	224746 bp	DNA	HTG	30-DEC-1998
RESULT					
LOCUS	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from				
DEFINITION	clone Y56A3, WORKING DRAFT SEQUENCE.				
ACCESSION	AL022280				

NID 94090202
 VERSION AL022280.1 GI:4090202
 KEYWORDS HTG: HTGS-PHASE1.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 224746)
 Sulston, J.
 Direct Submission
 Submitted (30-DEC-1998) Nematode Sequencing Project, Sanger Centre,
 Hinxton, Cambridge CB10 1RO, UK and Department of Genetics,
 Washington University, St. Louis, MO 63110, USA. E-mail:
 jes@sanger.ac.uk or rwnematode.wustl.edu
 On Dec 31, 1998 this sequence version replaced gi:4006996.
 IMPORTANT: This sequence is unfinished and does not necessarily
 represent the correct sequence. Work on the sequence is in progress
 and the release of this data is based on the understanding that the
 sequence may change as work continues. The sequence may be
 contaminated with foreign sequence from E.coli, yeast, vector,
 phage etc. Order of segments is not known; 800 n's separate
 segments.
 * NOTE: This is a 'working draft' sequence.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES
 Location/Qualifiers

1..224746
 /organism="Caenorhabditis elegans"
 /db_xref="taxon:6239"
 /chromosome="III"
 /clone="Y56A3"

BASE COUNT 67718 a 40130 c 41166 g 69255 t 6477 others

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 Best Local Similarity 100.0%; Pred. No. 1.25e-33;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 136606 GC AAAATATCTCGTAGCGAAACACAGTAACTTTAAATGACTAGTGGCTGTG 136665
 QY 1394 GC AAAATATCTCGTAGCGAAACACAGTAACTTTAAATGACTAGTGGCTGTG 1453
 Db 136666 TCGATTACGGGC 136678
 QY 1454 TCGATTACGGGC 1466

RESULT 5
 LOCUS AC006766 4917 bp DNA HTG 23-FEB-1999
 DEFINITION Caenorhabditis elegans clone Y44E3B, WORKING DRAFT SEQUENCE, 1
 unorderd pieces.
 ACCESSION AC006766
 NID 94263172
 VERSION AC006766.1 GI:4263172
 KEYWORDS HTG; HTGS-PHASE1.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 4917)
 Waterston, R.H.
 The sequence of Caenorhabditis elegans clone
 Unpublished
 REFERENCE 2 (bases 1 to 4917)
 JOURNAL Waterston, R.H.
 TITLE Direct Submission
 AUTHORS Waterston, R.H.
 Submitted (23-FEB-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES
 Location/Qualifiers

1..4917
 /organism="Caenorhabditis elegans"
 /db_xref="taxon:6239"
 /clone="Y44E3B"

BASE COUNT 1381 a 977 c 1003 g 1556 t

ORIGIN

Query Match 0.9%; Score 71; DB 19; Length 4917;
 Best Local Similarity 100.0%; Pred. No. 4.31e-32;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 2646 CGCTAATCGACACACAGCGCTACAGTAGTCATTAAAGAAATTTAGCTAGCTAGC 2705
 Cp 1464 CGCTAATCGACACACAGCGCTACAGTAGTCATTAAAGAAATTTAGCTAGCTAGC 1405
 Db 2706 AGATATTTCG 2716
 Cp 1404 AGATATTTCG 1394

RESULT 6
 LOCUS CELY44E3B 4917 bp DNA INV 05-MAR-1999
 DEFINITION Caenorhabditis elegans cosmid Y44E3B.
 ACCESSION AF078789
 NID 9329615
 VERSION AF078789.1 GI:3329615
 KEYWORDS
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 4917)
 Wilson, R., Alnsough, R., Anderson, K., Baynes, C., Berks, M.,
 Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
 Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
 Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
 Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
 Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
 O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roodra, A.,
 Saunders, D., Showkeen, R., Smalton, N., Smith, A., Sonhammer, E.,
 Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
 Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
 Wilkinson-Sproat, J. and Wohlman, P.
 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans

TITLE
 JOURNAL Nature 368 (6466), 32-38 (1994)
 MEDLINE 94150718
 REFERENCE 2 (bases 1 to 4917)
 AUTHORS Woessner, J., Graves, T. and Keppler, D.
 TITLE The sequence of C. elegans cosmid Y44E3B
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 4917)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Waterston, R.
 Submitted (16-JUL-1998) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 4 (bases 1 to 4917)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Waterston, R.
 Submitted (20-OCT-1998) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 5 (bases 1 to 4917)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Waterston, R.
 Submitted (05-MAR-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

Submitted by:
 Genome Sequencing Center
 Department of Genetics, Washington University,
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1RQ, England
 e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

This is a segment of YAC Y44E3, sequenced to span the gap between Y54E10A and W01B11. The 5' clone is Y54E10A; 3' clone is W01B11, 200 bp overlap. Actual start of YAC Y44E3 is at base position 1 of CELY44E3B; actual end is at 10513 of CELK03E5

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation). Location/Qualifiers

FEATURES

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source
1..4917
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="Y44E3B"
/chromosome="I"
363..3080
/gene="Y44E3B.2"
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1526..1629,2867..3080)
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/note="contains similarity to the common central domain of
tyrosinases, polyphenol oxidases and some hemocyanins
(Pfam: tyrosinase.hmm, score: 97.33)"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC64634.1"
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NRFGEEDSGMLNDARVLIINPDINILGATWPLSCPNHILDRALFEFSDYVH
FVNGDMKSYSSNDVCFVYHGMIDWIFEHWRNOMOSREERTEPKSDRCFPFW
HNGDMSPLLPKLNKDALSDNYEYPRPTCTRENPDGSPYLCFYIPNNEH
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complement(join(3375..3447,3500..4257,4699..4824))
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/note="contains similarity to the basic region plus the
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for by C. elegans cDNA yk437c3.5; coded for by C. elegans
cDNA yk437c3.3"
/codon_start=1
/protein_id="AAC64635.1"
/db_xref="PID:g3329617"
/db_xref="GI:3329617"

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 TRRAIKRPSYDDYQEEGETSLSDNDSVDSYKPKSKKRYTAAVAFNPFVKTKARKY
 NLKPDKEVEPIYKLRARNNDAYKSRNKAKELOKQDEYDEMKKRITQLEAELOS
 EREGREDQQLIKOLIREKESTSGPKRKSRRNALESFNKSNY"

BASE COUNT 1381 a 977 c 1003 g 1556 t
 ORIGIN

Query Match 0.9%; Score 71; DB 22; Length 4917;
 Best Local Similarity 100.0%; Pred. No. 4.31e-32;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2646 CCCTAATCGACACACGCGTACAGTAGTCATTAAAGAAATTACTGTCTTCCTAGC 2705
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Cp 1464 CCCTAATCGACACACGCGTACAGTAGTCATTAAAGAAATTACTGTCTTCCTAGC 1405
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Db 2706 AGATATTTTGC 2716
 |||||||||||

Cp 1404 AGATATTTTGC 1394

RESULT 7

LOCUS AC006696 38846 bp DNA HTG 23-FEB-1999
 DEFINITION Caenorhabditis elegans clone W08E12, WORKING DRAFT SEQUENCE, 1
 unorderd pieces.

ACCESSION AC006696

NID 94263242

VERSION AC006696.1 GI:4263242

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE 1 (bases 1 to 38846)
 Waterston,R.H.
 The sequence of Caenorhabditis elegans clone

TITLE Unpublished

JOURNAL 2 (bases 1 to 38846)

REFERENCE Waterston,R.H.

AUTHORS Direct Submission

TITLE Submitted (23-FEB-1999) Genome Sequencing Center, Washington

JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved

* 1 38846: contig of 38846 bp in length.

FEATURES

source Location/Qualifiers

1..38846

/organism="Caenorhabditis elegans"

/db_xref="taxon:6239"

/clone="W08E12"

BASE COUNT 11655 a 8013 c 7662 g 11516 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.36e-33;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20039 GAGCCGCTAAATCGACACACGCGTACAGTAGTCATTAAAGAAATTACTGTCTTCGC 20098
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Cp 1468 GAGCCGCTAAATCGACACACGCGTACAGTAGTCATTAAAGAAATTACTGTCTTCGC 1409
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Db 20099 TACGAGATATT 20110
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Cp 1408 TACGAGATATT 1397

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8
RESULT LOCUS      CEP53A2      42724 bp      DNA      INV      18-DEC-1998
DEFINITION Caenorhabditis elegans cosmid F53A2, complete sequence.
ACCESSION  Z81546
NID         92853125
VERSION     281546.1  GI:2653125
KEYWORDS   HTG.
SOURCE     Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans.
REFERENCE  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
AUTHORS    Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
TITLE      1 (bases 1 to 42724)
JOURNAL    Direct Submission
LLOYD,C.
Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail:
jesanger.ac.uk or rwnematode.wustl.edu
2 (bases 1 to 42724)
Wilson,R., Ainscough,R., Anderson,K., Raynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifkin,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smalton,N., Smith,A., Sonhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohlman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
JOURNAL    Nature 368 (6466), 32-38 (1994)
MEDLINE    94150718
COMMENT    On Nov 29, 1997 this sequence version replaced gi:1914312.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
For a graphical representation of this sequence and its analysis
see:-
http://webcace.sanger.ac.uk/cgi-
bin/display?db=wormacsc&seq=Sequence &object=F53A2
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
This sequence is the entire insert of clone F53A2. The start of
this sequence (1..104) overlaps with the end of sequence AL021481.
The end of this sequence (42621..42724) overlaps with the start of
sequence Z99272.
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FSGCVRSPTKQDCGFSAMQVLYRVLKDNTNIMPACQFTGTGTSQKLLSFQKEDSLNNV
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yk403a12.3 comes from this gene; cDNA EST yk403a12.5 comes
from this gene; cDNA EST yk392g11.3 comes from this gene;
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yk391a2.5 comes from this gene; cDNA EST EMBL:D7147 comes from this gene;
cDNA EST EMBL:T00154 comes from this gene; cDNA EST
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 YK385E3.5 comes from this gene; CDNA EST YK425G1.3 comes
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 Note: remainder of annotations omitted.

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 Best Local Similarity 100.0%; Pred. No. 1.46e-30;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 1399 ATATCTCTAGCGAAACTACAGTAATCTTTAAATGACTACTAGCGCTTGTCGAT 1458
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 Db 37810 TTACGGGCT 37818
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 Qy 1459 TTACGGGCT 1467

RESULT 9

LOCUS
 DEFINITION
 ACCESSION
 NID
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

TITLE

JOURNAL
 MEDLINE
 REFERENCE
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

CELFS9B1 43152 bp DNA INV 29-MAY-1998
 Caenorhabditis elegans cosmid F59B1.
 AF067943
 93165541
 AF067943.1 GI:3165541

Caenorhabditis elegans.

Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 43152)

Willson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
 Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
 Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
 Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
 Johnston,L., Jones,A., Kershaw,J., Kirsten,J., Laister,N.,
 Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
 O'Callaghan,M., Parsons,J., Percy,C., Rifkin,L., Roopra,A.,
 Saunders,D., Showkeen,R., Smalton,N., Smith,A., Sonnhammer,E.,
 Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
 Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
 Wilkison-Sproat,J. and Wohlman,P.
 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

elegans
 Nature 368 (6466), 32-38 (1994)

94150718

2 (bases 1 to 43152)

Wu.X.

The sequence of C. elegans cosmid F59B1

Unpublished (1998)

3 (bases 1 to 43152)

Waterston,R.

Direct Submission

Submitted (23-MAY-1998) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

Submitted by:

Genome Sequencing Center
 Department of Genetics, Washington University,
 St. Louis, MO 63110, USA, and
 Sanger Centre, Hinxton Hall
 Cambridge CB10 1HQ, England
 e-mail: rw@ematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we provide a small overlap between
 neighboring submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded or sequenced with an alternate
 chemistry; an attempt was made to resolve all sequencing problems,
 such as compressions and repeats; all regions were covered by
 sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is M01F7, 200 bp overlap. Actual start of this
 cosmid is at base position 1 of CELF59B1; actual end is at 43152 of
 CELF59B1

NOTES:

Coding sequences below are predicted from computer analysis, using
 the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES
 Source

Location/Qualifiers
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NLWFDNPSVHDVSVSNQRMILILMLIFSGFMYSLLYIMVLVLEISQATSKSLK
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NCNLPYDFGWTFGVNSADCDVIRFYDFCDGFGVVALIADVGTIVYIKVTAPGM
KLLSANCASQKRRQREITFVQALIQGAVFATLIVFFFIISGMSQPVYAIELCTTVA
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Note: remainder of annotations omitted.

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Db 13815 TCGATTACGGG 13826
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QY 1454 TCGATTACGGG 1465

RESULT 10
LOCUS CELF59B1 43152 bp DNA INV 29-MAY-1998
DEFINITION Caenorhabditis elegans cosmid F59B1.

ACCESSION NID VERSION KEYWORDS SOURCE ORGANISM	AF067943 g3165541 AF067943.1 GI:3165541 Caenorhabditis elegans. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Secernentes; Rhabditia; Rhabditida; Rhabditina; Rhabditidae; Pelodierinae; Caenorhabditis. 1 (bases 1 to 43152) Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsley, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Showkeen, R., Smaldon, N., Smith, A., Sonhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans Nature 368 (6466), 32-38 (1994) 94150718 2 (bases 1 to 43152) Wu, X. The sequence of C. elegans cosmid F59B1 Unpublished (1998) 3 (bases 1 to 43152) Waterston, R. Direct Submission Submitted (23-MAY-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA Submitted by: Genome Sequencing Center Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 1RQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk	CDS	<pre> /gene="F59B1.3" complement(join(2823..3071,3121..3287,3338..3570, 3617..3780,3827..3889)) /gene="F59B1.3" /note="contains similarity to seven trans-membrane receptors (Pfam: 7tm_1.hmm, score: 11.62)" /codon_start=1 /evidence=not_experimental /protein_id="AAC17662.1" /db_xref="PID:g3165545" /db_xref="GI:3165545" /translation="MSOEYNTDPLNLVAFLLGTIGTGVWCNSLIYIFLKEKSEQ TAFNVICFFRAISNVIIITLITLYLPKLLGVSYPYPAIESWFINTSPLYLGNEX QIVLMAINRCAMFFPKYSRISLSHTTIIILVLYRIAQKIYEWLPESAGCVTL FSTYFAWKYSAPGCDYDGAPEVIKYITFTAFNLNFIIFLILHFKKSNSSOVAV EAKRMKRNILNFIQTLLDLSLIDITFTFLRFVDFITFLKHKFKQFLEHSPCV DIFLWNYFLGMPTFS" /complement(5565..6879) /gene="F59B1.5" complement(join(5565..5727,5810..5844,6104..6270, 6326..6558,6603..6766,6817..6879)) /gene="F59B1.5" /note="contains similarity to melatonin receptors" /codon_start=1 /evidence=not_experimental /protein_id="AAC17665.1" /db_xref="PID:g3165548" /db_xref="GI:3165548" /translation="MSOEYNTDPLNLVAFLLGTIGTGVWCNALIYVFFKEKSKR TAFNVICFFRAISNVIIITLITLYLPKLLGVSYPYPAIESWFINTSPLYLGNEX QIVLMAINRCAMFFPKYSRISLSHTTIIILVLYRIAQKIYEWLPESAGCVTL FSTEDFYKYLISAPDCDMDNAPKLIKTYIATLAINFIITFLKILHFKLEHYPFVD IFLFIIMIFNKKLAPLTKTKKKKIVLPIGGHPRQQTSTVTTSYGNNTFVNN" /complement(8203..10225) /gene="F59B1.4" complement(join(8203..8304,8359..8472,8520..8636, 9707..9955,10007..10225)) /gene="F59B1.4" /codon_start=1 /evidence=not_experimental /protein_id="AAC17664.1" /db_xref="PID:g3165547" /db_xref="GI:3165547" /translation="MDNRVYATVHLTDRTLOLYLTNINCLATPWNFLAFYLIKHRS RETKLPKYLIIISHLFFVSNIEYCTIANNLINFWSAAIWFELFAGFVYFTMILVY RKIVARRGKTFDSNRSYIFCVILALYIIGPISATWIRSKYCTDQOIAVVTSEPK NLMVFDNPSVHDVSNORMIILMLILIFSGEMISLILMLIVLSEIKQATSKSLK TTNHQRKVTNSMVFQILIVGTTFVFPALLOLRNAPVEPEEDTRGNWQ" /complement(12634..14872) /gene="F59B1.6" complement(join(12634..12826,13056..13140,13183..13296, 13414..13687,14051..14149,14558..14872)) /gene="F59B1.6" /note="contains similarity to NADH-ubiquinone/plastoquinone domains (Pfam: oxidored_g1.hmm, score: 13.37)" /codon_start=1 /evidence=not_experimental /protein_id="AAC17661.1" /db_xref="PID:g3165544" /db_xref="GI:3165544" /translation="MNNFSVNSHFFAVIENDNRSLOPLMLNLINVIITIVFILIYAI ISRRKKESQIYQIVLITHTCWLQSVWGFSLSLVEFPFPGYIGYGLAPLSSY VLIIWILFAITVTFMIIILRLRGVTRKNSNFYSTAYSIFSAFAMVIAIPMP FCWISAGSISSETDFVRKFPNATKLDIPGIVYDTSWFKHRLVYVAVLLYGGV VSEFLKLSQQAHLMSNMHNLNPAAMOTLERENSKISQKSAERIDYSELTVHVC SNPTFGNSQICQPRGGHNYHDNHRNFCIVSNLRHNNILSKHTIOAGCNNVVSCS TOTAKCGIDYSFGSGSTNLIIFKSE" 16526..17717 /gene="F59B1.2" join(16526..16623,16705..16900,17053..17121,17595..17717) /gene="F59B1.2" /codon_start=1 </pre>	gene
FEATURES source	<p>NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.</p> <p>This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone</p> <p>NEIGHBORING COSMID INFORMATION:</p> <p>The 5' cosmid is M01F7, 200 bp overlap. Actual start of this cosmid is at base position 1 of CELF59B1; actual end is at 43152 of CELF59B1</p> <p>NOTES:</p> <p>Coding sequences below are predicted from computer analysis, using the program GeneFinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers 1..43152 /organism="Caenorhabditis elegans" /strain="Bristol N2" /db_xref="taxon:6239" /clone="F59B1" /chromosome="v" complement(2823..3889)</p>	CDS	<pre> /gene="F59B1.2" complement(join(16526..16623,16705..16900,17053..17121,17595..17717)) </pre>	gene

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KLLSACAOQKQRREITFVKQALIQGAFVATLVEFRIISGMOSQPVAILCTTVA
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GMEYVSGSIVRSYDCTEETQPIRLAKLQALSLQNPALSKDLQIDNGAIFQE
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LKGIFDQSRNIDKLSKVERTEQNHKEILNLETLNLYVVDKQVICHGDLWAF
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gene 32954..34638
Note: remainder of annotations omitted.

Query Match 0.9%; Score 72; DB 21; Length 43152;
Best Local Similarity 100.0%; Pred. No. 7 36e-33;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14024 GAGATATTTGC 14035
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Cp 1405 GAGATATTTGC 1394

RESULT 11
LOCUS CELY44E3A 48088 bp DNA INV 05-MAR-1999
DEFINITION Caenorhabditis elegans cosmid Y44E3A.
ACCESSION AF106589
NID 93886084
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AF106589.1 GI:3886084
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
Wilson, R., Alnsough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
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Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
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Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J., and Wohlman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
Nature 368 (6466), 32-38 (1994)
2 (bases 1 to 48088)
Woessner, J., Graves, T. and Keppler, D.
The sequence of C. elegans cosmid Y44E3A
unpublished
3 (bases 1 to 48088)
Waterston, R.
Direct Submission
Submitted (15-NOV-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 48088)
Waterston, R.
Direct Submission
Submitted (05-MAR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, UK
e-mail: r.w@nematoe.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

This segment of YAC Y44E3 was sequenced to span the gap between
W01B1 and W05F2. The 5' clone is W01B1, 200 bp overlap; 3' clone
is W05F2, 2300 bp overlap. Actual start of YAC Y44E3 is at base
position 1 of CELY44E3B; actual end is at 10513 of CELK03E5

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).

Location/Qualifiers
1. 48088
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/strain="Bristol N2"

FEATURES
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ELQHIKRNARPKNPKPMVMNRSSDESNGRLSSPTSTSYNPMASAFVATA
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... Note: remainder of annotations omitted.

Query Match	Score	DB	Length
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Mismatches	0	Indels	0
Gaps	0		

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 QY 1454 TCGATTACGGG 1465

RESULT 12 AC006891 178553 bp DNA HTG 24-FEB-1999
 LOCUS Caenorhabditis elegans clone y67D8y, WORKING DRAFT SEQUENCE, 3
 DEFINITION unordered pieces.
 ACCESSION AC006891
 NID 94263457
 VERSION AC006891.1 GI:4263457

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47071..47218,47852..47997))
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(GI:U17474); coded for by C. elegans cDNA yk257g3.3; coded
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cDNA yk133b11.3; coded for by C. elegans cDNA yk285a7.3;
coded for by C. elegans cDNA CEESK35RB; coded for by C.
elegans cDNA CEESK35R; coded for by C. elegans cDNA
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VLFRLNEHFRHGINEYLAATTSQIGTAMATQMAAQOQKQGLERIALLRMIETN
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Mon Aug 9 13:54:53 1999

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* 5449 5463: gap of unknown length
* 5464 14405: contig of 8942 bp in length
* 14406 14420: gap of unknown length
* 14421 28085: contig of 13665 bp in length
* 28086 28100: gap of unknown length
* 28101 84320: contig of 56220 bp in length
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            /db_xref="taxon:6239"
            /clone="Y39H10"
BASE COUNT 77112 a 45383 c 45498 g 77737 t 75 others
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    Query Match 0.9%; Score 72; DB 20; Length 245805;
    Best Local Similarity 100.0%; Pred. No. 7.36e-33;
    Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 193472 CCCGTAATCGACACAGCGCTACAGTACATTTAAAGAAATTAAGTATTTTCGCTAC 193531
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Cp 1465 CCCGTAATCGACACAGCGCTACAGTACATTTAAAGAAATTAAGTATTTTCGCTAC 1406
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|
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Cp 1405 GAGATATTTTGC 1394
|
|
|
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DEFINITION Caenorhabditis elegans clone Y67D8x, WORKING DRAFT SEQUENCE, 23
unordered pieces.
ACCESSION AC006890
NID 94263458
VERSION AC006890.1 GI:4263458
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.
Waterston,R.H.
The sequence of Caenorhabditis elegans clone
2 (bases 1 to 298195)
Unpublished
Waterston,R.H.
Direct Submission
Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 2711: contig of 2711 bp in length
* 2712 2725: gap of unknown length
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* 7190 9231: contig of 2042 bp in length
* 9232 9245: gap of unknown length
* 9246 13485: contig of 4240 bp in length
* 13486 13499: gap of unknown length
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* 25109 25122: gap of unknown length

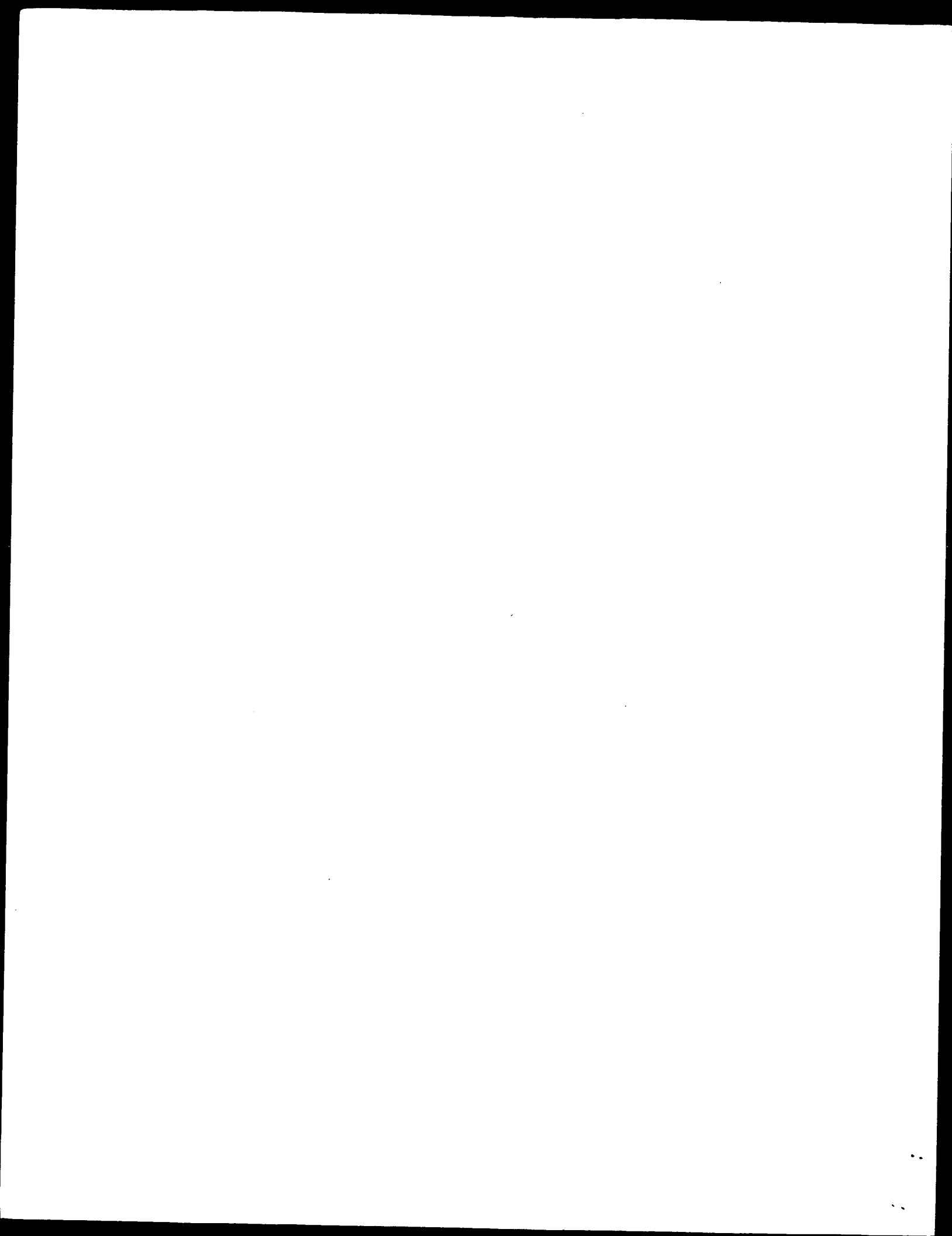
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87	18	0.2	20	9	Q49455	Primer for detecting	7.21e+01	160	18	0.2	32	5	Q34149	Sequence of a microsa	7.21e+01
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289	18	0.2	51 29	T65715	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
290	19	0.2	51 5	Q34071	Microsatellite sequen	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
291	18	0.2	52 29	T66069	(dc-da)n.(dg-dt)n pol	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
292	18	0.2	52 29	T66108	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
293	18	0.2	53 29	T65768	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
294	19	0.2	54 5	Q33870	Microsatellite sequen	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
295	18	0.2	54 11	Q45388	Oligonucleotide formi	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
296	18	0.2	55 5	Q33864	Microsatellite sequen	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
297	19	0.2	56 29	T65735	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
298	19	0.2	56 29	T65707	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
299	18	0.2	56 29	T66063	(dc-da)n.(dg-dt)n pol	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
300	18	0.2	56 29	T65769	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01
301	18	0.2	56 29	T65796	Repeat sequence from	7.21e+01	18	0.2	60	29	T65762	Repeat sequence from	1.97e+01

521	19	0.2	489 30	T72059	Sequence flanking mar	1.97e+01	18	0.2	1275 56	V84529	Human secreted protei	7.21e+01
522	18	0.2	500 60	X13700	Enterococcus faecalis	7.21e+01	18	0.2	1302 24	T43045	Helicobacter pylori p	7.21e+01
523	18	0.2	502 7	Q46914	Human Kunitz-type pro	1.97e+01	18	0.2	1307 56	V84569	Human secreted protei	7.21e+01
524	18	0.2	508 53	Q69714	3' portion of intron	7.21e+01	18	0.2	1325 42	V28088	Mus musculus vascular	7.21e+01
525	18	0.2	537 60	X13917	Enterococcus faecalis	7.21e+01	18	0.2	1329 50	V33199	Secreted protein FB78	7.21e+01
526	19	0.2	543 16	Q85537	DNA probe 43 detects	1.97e+01	18	0.2	1371 52	V33755	Mouse neutrophil elas	7.21e+01
527	19	0.2	545 30	T43932	Sequence flanking mar	1.97e+01	18	0.2	1400 12	Q70142	Human cartilage link	1.97e+01
528	19	0.2	547 38	T72052	Sequence flanking mar	1.97e+01	18	0.2	1427 41	V05663	Human cathepsin K gen	1.97e+01
529	18	0.2	557 38	Q61558	Tumour suppression ge	7.21e+01	18	0.2	1429 17	T09625	Neurotrophin-6 cDNA	1.97e+01
530	19	0.2	560 2	N60553	Fragment of plasmid p	1.97e+01	18	0.2	1442 19	Q98919	TGF-beta inducible re	1.97e+01
531	18	0.2	560 1	Q06235	Bovine male-specific	7.21e+01	18	0.2	1470 30	T72063	Sequence flanking mar	1.97e+01
532	18	0.2	571 28	T33598	Mouse fibrosin cDNA	1.97e+01	18	0.2	1470 30	T43943	Sequence flanking mar	1.97e+01
533	18	0.2	571 28	T61383	Mouse fibrosin cDNA	7.21e+01	18	0.2	1493 5	Q28411	Glia activating facto	1.97e+01
534	19	0.2	585 43	T28925	Bison Nramp1 DNA SEQ	1.97e+01	18	0.2	1517 51	V59788	Human secreted protei	7.21e+01
535	19	0.2	587 43	V28928	Bison Nramp1 DNA SEQ	1.97e+01	18	0.2	1528 26	T45972	Mouse utrophin gene p	7.21e+01
536	19	0.2	592 15	Q85520	DNA probe 26 detects	1.97e+01	18	0.2	1533 30	T71575	Exon 1 of LETO rat ch	7.21e+01
537	18	0.2	594 53	V88419	EST clone EK634	7.21e+01	18	0.2	1542 25	T21732	DNA encoding a RAP-2	7.21e+01
538	18	0.2	597 16	Q92942	Natural resistance-as	7.21e+01	18	0.2	1548 1	N80038	Male-specific cDNA seq	7.21e+01
539	19	0.2	600 30	T43950	Sequence flanking mar	1.97e+01	18	0.2	1557 50	V46430	Colony stimulating ge	7.21e+01
540	18	0.2	605 30	T72055	Sequence flanking mar	7.21e+01	18	0.2	1560 37	T88012	Region upstream of co	7.21e+01
541	18	0.2	605 30	T43935	Sequence flanking mar	7.21e+01	18	0.2	1579 47	V41689	Murine osteocalcin B q	7.21e+01
542	18	0.2	637 22	T18874	Human survival motor	7.21e+01	18	0.2	1579 47	V41689	Murine osteocalcin B q	7.21e+01
543	18	0.2	672 30	T43948	Sequence flanking mar	7.21e+01	18	0.2	1586 60	X00238	Murine CD3delta T cel	1.97e+01
544	18	0.2	688 30	T43940	Sequence flanking mar	1.97e+01	18	0.2	1606 17	T01050	Murine CD3delta T cel	1.97e+01
545	18	0.2	698 38	V06140	Sequence flanking mar	7.21e+01	18	0.2	1614 24	T40206	Mouse B7-1 exons 1, 2	7.21e+01
546	19	0.2	704 49	V61632	Human TACE-like DNA	1.97e+01	18	0.2	1647 9	Q52272	Tobacco lycopene cycl	7.21e+01
547	18	0.2	705 30	T72057	Sequence flanking mar	1.97e+01	18	0.2	1679 35	Q27106	Human checkpoint gene	7.21e+01
548	19	0.2	705 30	T43937	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Human RADcompB cDNA s	7.21e+01
549	19	0.2	724 30	T72064	Sequence flanking mar	1.97e+01	18	0.2	1686 7	Q43957	Bone morphogenetic pr	7.21e+01
550	19	0.2	724 30	T43944	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	cDNA encoding human z	7.21e+01
551	19	0.2	724 30	T43944	Sequence flanking mar	1.97e+01	18	0.2	1686 7	Q43957	cDNA encoding human z	7.21e+01
552	18	0.2	751 30	T43931	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Gastrin releasing pep	1.97e+01
553	18	0.2	751 30	T72051	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Encodes gastrin relea	1.97e+01
554	19	0.2	761 19	Q98920	TGF-beta inducible re	1.97e+01	18	0.2	1686 7	Q43957	Mouse RIBP (GRP-R)	1.97e+01
555	19	0.2	766 52	V65399	Promoter sequence of	1.97e+01	18	0.2	1686 7	Q43957	Human secreted protei	7.21e+01
556	18	0.2	780 30	T43181	5'ALT DNA sequence co	7.21e+01	18	0.2	1686 7	Q43957	Mouse uncoupling prot	7.21e+01
557	18	0.2	818 17	T01034	Mouse B7-1 exon 6 (Cy	1.97e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
558	18	0.2	829 42	V29366	Calcium ion channel a	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
559	18	0.2	835 38	V06122	Viral infection gene	1.97e+01	18	0.2	1686 7	Q43957	Prepro human CBMP2B c	7.21e+01
560	19	0.2	848 2	Q13632	GBMT modified transcr	1.97e+01	18	0.2	1686 7	Q43957	Human CBMP2(b) cDNA	7.21e+01
561	18	0.2	867 35	T66791	Partial seq. obtained	7.21e+01	18	0.2	1686 7	Q43957	Sequence encoding ost	7.21e+01
562	18	0.2	875 49	V58364	Coding sequence for s	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
563	18	0.2	882 22	T14630	Tie receptor tyrosine	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
564	18	0.2	884 38	V06156	Tumour suppression ge	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
565	18	0.2	970 55	V08841	Gene No. 31 encoding	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
566	18	0.2	972 30	T68932	Bovine PIT-1 exon 6 s	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
567	18	0.2	1000 30	T72062	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
568	18	0.2	1000 30	T43942	Sequence flanking mar	1.97e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
569	19	0.2	1016 12	Q70049	Dirofilaria immitis p	1.97e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
570	19	0.2	1045 30	T72058	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
571	19	0.2	1045 30	T72058	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
572	18	0.2	1050 30	T43927	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
573	18	0.2	1050 30	T72047	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
574	18	0.2	1091 60	X13502	Enterococcus faecalis	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
575	18	0.2	1139 1	N90255	Interleukin-6	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
576	18	0.2	1139 1	N80299	Interleukin-6	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
577	18	0.2	1166 30	T43941	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
578	18	0.2	1166 30	T72061	Sequence flanking mar	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
579	19	0.2	1176 2	Q10063	Bovine Y-specific seq	1.97e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
580	18	0.2	1194 2	N70395	Sequence encoding rat	1.97e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
581	19	0.2	1199 6	Q36051	Human nov gene promot	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
582	18	0.2	1215 28	T58339	Tobacco epi-5-aristol	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
583	19	0.2	1217 3	N40211	DNA sequence encoding	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
584	18	0.2	1231 38	T95755	Arabidopsis SCARECROW	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
585	18	0.2	1245 7	Q41102	HME1	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
586	18	0.2	1245 44	V35607	Human mammary epithel	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
587	18	0.2	1249 1	Q06091	Murine cellular enhan	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
588	18	0.2	1257 2	N70394	Sequence encoding hum	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
589	18	0.2	1260 30	T72049	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
590	18	0.2	1260 30	T43929	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
591	18	0.2	1260 30	T72045	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
592	18	0.2	1260 30	T43925	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01
593	18	0.2	1260 30	T43925	Sequence around marke	7.21e+01	18	0.2	1686 7	Q43957	Human osteogenic prot	7.21e+01

C 667	18	0.2	2029	3	Q20495	PN-I alpha analogue, 7.21e+01	19	0.2	2703	29	T59729	Human bone morphogeni	1.97e+01
C 668	18	0.2	2031	15	O89925	Protease Nexin-1 type 7.21e+01	19	0.2	2703	38	T98191	cDNA for human MP52,	1.97e+01
C 669	18	0.2	2031	1	N81282	Sequence of coding re 7.21e+01	19	0.2	2703	38	T61412	cDNA encoding human p	1.97e+01
C 670	18	0.2	2032	3	Q22587	PN-I beta analogue, P 7.21e+01	19	0.2	2703	36	T69695	DNA encoding human TG	1.97e+01
C 671	18	0.2	2032	3	Q22586	PN-I beta analogue, P 7.21e+01	19	0.2	2703	36	T88340	Human MP52 cDNA.	1.97e+01
C 672	18	0.2	2032	3	Q22585	PN-I beta analogue, P 7.21e+01	19	0.2	2703	39	T86340	Human MP52 cDNA.	1.97e+01
C 673	19	0.2	2032	52	V34207	Human secreted protei 1.97e+01	19	0.2	2703	32	T59405	DNA encoding human MP	1.97e+01
C 674	18	0.2	2040	50	V57558	Mouse SNAP-25 polypep 7.21e+01	19	0.2	2712	34	T38265	200 gene differential	1.97e+01
C 675	18	0.2	2040	38	V01554	Mouse synaptosomal-as 7.21e+01	18	0.2	2732	14	O84559	Murine C140 receptor	7.21e+01
C 676	18	0.2	2040	30	T433949	Sequence flanking mar 7.21e+01	18	0.2	2732	27	T32038	Murine C140 receptor	7.21e+01
C 677	18	0.2	2057	29	T63123	Human metalloproteina 7.21e+01	18	0.2	2746	55	V72893	Rabbit protein-couple	7.21e+01
C 678	18	0.2	2075	28	T45360	Human connective tiss 7.21e+01	19	0.2	2752	43	V11736	Barley alpha-glucosid	7.21e+01
C 679	18	0.2	2075	44	V38085	Human connective tiss 7.21e+01	19	0.2	2757	30	T43936	Sequence flanking mar	1.97e+01
C 680	18	0.2	2075	18	T04226	Connective tissue gro 7.21e+01	18	0.2	2757	30	T72056	Sequence flanking mar	1.97e+01
C 681	18	0.2	2075	26	T51234	Connective tissue gro 7.21e+01	18	0.2	2764	31	T43351	G-protein coupled rec	7.21e+01
C 682	18	0.2	2085	44	V32028	Nucleotide sequence o 7.21e+01	18	0.2	2775	25	T47511	Rat androgen receptor	7.21e+01
C 683	18	0.2	2099	47	V51370	Human TIGR exon 3 DNA 7.21e+01	18	0.2	2783	15	Q92367	Chick p75 cDNA.	7.21e+01
C 684	18	0.2	2107	33	T86264	Rat brain Neuroglycan 7.21e+01	18	0.2	2838	57	V83507	Killer cell activator	7.21e+01
C 685	18	0.2	2110	7	Q41228	Clone GP22 encoding m 7.21e+01	18	0.2	2838	57	V83507	Killer cell activator	7.21e+01
C 686	18	0.2	2116	46	V32619	Mouse preprotachykin 7.21e+01	18	0.2	2858	13	Q52700	Unique 2.9 kb genomic	7.21e+01
C 687	19	0.2	2136	52	V34263	Human secreted protei 1.97e+01	18	0.2	2866	27	T43383	Human cytokine respon	7.21e+01
C 688	19	0.2	2160	11	Q66641	Mouse Activin recepto 7.21e+01	18	0.2	2892	5	Q30997	Human cytokine respon	7.21e+01
C 689	18	0.2	2166	24	T82332	Apoptosis-regulating 7.21e+01	19	0.2	2919	30	T51124	Delta cDNA Dll.	7.21e+01
C 690	18	0.2	2182	3	Q08510	Sequence of anylase g 7.21e+01	19	0.2	2947	40	V18821	Human homeoprotein re	1.97e+01
C 691	18	0.2	2186	50	V57441	Human tumour necrosis 7.21e+01	19	0.2	2956	37	T99140	Murine hyaluronan syn	1.97e+01
C 692	19	0.2	2215	60	V99330	CDNA encoding a GDNFR 1.97e+01	18	0.2	2960	7	Q42561	Full length cytochrom	1.97e+01
C 693	18	0.2	2220	14	O84048	Insertion sequence pH 7.21e+01	18	0.2	2967	15	Q87171	Histamine H1 receptor	1.97e+01
C 694	18	0.2	2240	36	T30773	CD40 associated prote 7.21e+01	18	0.2	2972	20	T03574	Natural resistance-as	7.21e+01
C 695	18	0.2	2263	57	V80628	Kidney injury associa 7.21e+01	18	0.2	2995	57	V64417	Rat protocadherin pc5	7.21e+01
C 696	18	0.2	2271	43	V28936	Bovine Nramp1 encodin 7.21e+01	19	0.2	2997	17	T11641	Mouse developing live	1.97e+01
C 697	18	0.2	2298	47	T42548	Mouse dectin-1 cDNA. 7.21e+01	19	0.2	3000	38	V01547	Murine osteogenic pro	1.97e+01
C 698	19	0.2	2299	17	T11640	Murine osteogenic pro 1.97e+01	18	0.2	3025	6	Q39966	Rat syntaxin 1B gene.	1.97e+01
C 699	18	0.2	2308	6	Q35148	Rat D1B dopamine rece 7.21e+01	18	0.2	3046	44	V29074	PKC-gamma cDNA.	1.97e+01
C 700	18	0.2	2310	29	T47712	Mouse bone morphogene 7.21e+01	18	0.2	3048	40	V15294	Rattus norvegicus NRL	7.21e+01
C 701	18	0.2	2312	2	Q12020	Sequence of Wilms' tu 7.21e+01	18	0.2	3054	7	V42406	Murine AGP-1 encoding	7.21e+01
C 702	18	0.2	2312	2	Q12020	Wilms' tumour polypep 7.21e+01	18	0.2	3066	8	Q48985	Mouse lactoferrin gen	7.21e+01
C 703	18	0.2	2315	52	V34322	Arabidopsis thaliana 7.21e+01	18	0.2	3069	9	O51015	Rat glucagon-like pep	7.21e+01
C 704	18	0.2	2319	52	V64070	M. hyopneumoniae 2.3k 7.21e+01	18	0.2	3096	2	N71063	Rat opiod receptor g	7.21e+01
C 705	18	0.2	2334	39	V09695	DHR3 gene. 7.21e+01	19	0.2	3114	1	N80336	Genomic sequence enco	7.21e+01
C 706	19	0.2	2338	2	Q13575	Kidney injury associa 1.97e+01	18	0.2	3120	7	Q39261	Sequence encoding pro	1.97e+01
C 707	19	0.2	2349	57	V80608	Dehiscence zone-selec 7.21e+01	18	0.2	3120	7	Q39261	Human t-complex assoc	7.21e+01
C 708	18	0.2	2352	30	T63604	LMPI associated prote 7.21e+01	18	0.2	3134	30	T62135	Human t-complex assoc	7.21e+01
C 709	18	0.2	2359	22	T31273	3' UTR sequence of ie 7.21e+01	18	0.2	3134	48	V47555	Leishmania major M15	7.21e+01
C 710	18	0.2	2396	53	V69703	CDNA encoding a chime 7.21e+01	18	0.2	3171	12	Q72332	Deletated in polyposi	7.21e+01
C 711	18	0.2	2403	36	T97870	CDNA encoding a chime 7.21e+01	18	0.2	3172	37	T96154	Human TB2 gene.	7.21e+01
C 712	18	0.2	2412	36	T97869	Apoptosis participati 7.21e+01	18	0.2	3172	36	T95539	Human TB2 gene.	7.21e+01
C 713	18	0.2	2433	23	T29396	Human secreted protei 7.21e+01	18	0.2	3172	4	V56448	Human TB2 gene.	7.21e+01
C 714	18	0.2	2436	51	V59776	Rat biglycan cDNA. 1.97e+01	18	0.2	3172	4	Q27235	Encodes DPl gene in f	7.21e+01
C 715	19	0.2	2446	17	T08768	Human interleukin-11 7.21e+01	18	0.2	3190	6	Q38746	CD22-beta gene.	7.21e+01
C 716	18	0.2	2456	22	T33278	Arabidopsis HY4 cDNA 7.21e+01	18	0.2	3202	29	T47520	Human hepatoma-derive	1.97e+01
C 717	18	0.2	2458	17	T16306	Murine lymphoid enhan 7.21e+01	18	0.2	3216	51	V33493	DNA encoding a Staphy	7.21e+01
C 718	18	0.2	2460	30	T67106	EcoRI fragment encodi 7.21e+01	19	0.2	3223	11	Q66475	Inulinase coding sequ	1.97e+01
C 719	18	0.2	2463	3	Q20810	Human cocaine and amp 1.97e+01	18	0.2	3269	17	T06024	CDNA encoding avenaci	7.21e+01
C 720	19	0.2	2483	30	T45982	Human cocaine and amp 1.97e+01	18	0.2	3288	46	V27591	Mouse interleukin-17	7.21e+01
C 721	19	0.2	2483	49	V57895	Human cocaine and amp 7.21e+01	18	0.2	3288	23	T33800	Murine interleukin-17	7.21e+01
C 722	18	0.2	2485	4	Q25594	Rabbit Gnt I cDNA clo 7.21e+01	19	0.2	3316	47	V44859	Clone AQ73 coding s	1.97e+01
C 723	18	0.2	2492	13	Q79480	Thal catfish GHRH/PAC 7.21e+01	18	0.2	3358	49	V58005	Rat neuriturin recepto	7.21e+01
C 724	18	0.2	2497	10	Q55941	Murine leukaemia inhi 7.21e+01	18	0.2	3360	44	V19608	Mus musculus EPCR gen	7.21e+01
C 725	18	0.2	2498	4	Q25800	MLIF-R. 7.21e+01	19	0.2	3373	2	N80892	Sequence encoding new	7.21e+01
C 726	18	0.2	2498	9	Q58426	Mouse LIF-R clone 3. 7.21e+01	18	0.2	3381	46	V46298	C. reinhardtii protop	1.97e+01
C 727	18	0.2	2498	16	Q92271	Murine leukaemia inhi 7.21e+01	19	0.2	3381	46	V46298	C. reinhardtii protop	1.97e+01
C 728	19	0.2	2516	17	T01040	Mouse B7-1 exons 1, 2 1.97e+01	19	0.2	3381	33	T78597	Porphylin-accumulati	1.97e+01
C 729	18	0.2	2518	42	V23500	Human adrenaline beta 7.21e+01	18	0.2	3383	28	T60965	Porphylin-accumulati	1.97e+01
C 730	18	0.2	2529	21	T31531	Human secreted protei 7.21e+01	18	0.2	3402	23	T27310	Trypanosoma cruzi epi	7.21e+01
C 731	18	0.2	2529	35	T87468	Hamster Ubiquitin/S27 7.21e+01	18	0.2	3404	4	Q26683	Rat dopamine transpor	7.21e+01
C 732	18	0.2	2547	51	V61484	Human secreted protei 7.21e+01	18	0.2	3425	9	Q57072	AGE-modified DNA INS-	7.21e+01
C 733	19	0.2	2551	22	T30738	Rat cryptidin 3 gene. 1.97e+01	18	0.2	3468	28	T39486	CDNA sequence encodin	7.21e+01
C 734	18	0.2	2571	1	N81168	Fragment from clone e 7.21e+01	18	0.2	3480	47	V42046	Human steroidogenesi	7.21e+01
C 735	19	0.2	2573	46	V46297	C. reinhardtii protop 7.21e+01	18	0.2	3500	1	N90229	Anthrithum majus De	7.21e+01
C 736	18	0.2	2614	52	V65766	Rat progression eleva 1.97e+01	18	0.2	3519	1	Q05328	Mouse tumour necrosis	7.21e+01
C 737	18	0.2	2662	20	T08977	Actual shortened B-pe 7.21e+01	18	0.2	3531	57	V80591	Rat tumour necrosis f	1.97e+01
C 738	18	0.2	2666	45	V41101	Macrophage surface an 7.21e+01	18	0.2	3549	60	X13796	Kidney injury associa	7.21e+01
C 739	19	0.2	2703	14	Q83695	New TGF-beta family m 1.97e+01	18	0.2	3562	52	V60839	Enterococcus faecalis	7.21e+01

813	18	0.2	3573	1	N81065	Sequence of human thr	7.21e+01	18	886	18	0.2	5150	33	T78598	AS-30D tumour Type II	7.21e+01
814	19	0.2	3582	50	V62430	Prostate cancer antiq	1.97e+01	18	887	18	0.2	5153	21	T30347	Human YAP cDNA.	7.21e+01
815	18	0.2	3588	2	N70317	Sequence encoding por	7.21e+01	18	888	18	0.2	5232	48	V50338	Human XIAP coding seq	7.21e+01
816	18	0.2	3611	43	N84074	Murine GM-CSF encodin	7.21e+01	19	889	19	0.2	5232	25	T58225	DNA encoding inositol	1.97e+01
817	18	0.2	3640	1	V28424	Cloned p2.1 insert en	7.21e+01	18	890	18	0.2	5240	50	V48268	P. chrysogenum beta-N	7.21e+01
818	18	0.2	3680	56	V72671	Hamster BF-1 alpha tr	7.21e+01	18	891	18	0.2	5299	47	V51361	Human TIGR promoter r	7.21e+01
819	18	0.2	3680	22	T33559	Leukaemia inhibiting	7.21e+01	18	892	18	0.2	5300	47	V51366	Human TIGR promoter m	7.21e+01
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822	19	0.2	3699	3	Q33445	Vector pGPe.	1.97e+01	18	895	18	0.2	5300	47	V51362	Human TIGR promoter m	7.21e+01
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825	19	0.2	3699	7	Q44179	Plasmid pGPe #2.	1.97e+01	18	898	18	0.2	5543	50	T75284	Nucleotide sequence e	1.97e+01
826	19	0.2	3699	37	V02619	Plasmid pGPe #2.	1.97e+01	18	899	18	0.2	5543	50	T75284	Nucleotide sequence e	1.97e+01
827	18	0.2	3708	4	Q23963	Probe Bty2.	7.21e+01	18	900	18	0.2	5578	13	Q76023	TGF-beta-2 promoter r	7.21e+01
828	18	0.2	3727	42	V11126	Rat SH2 binding prote	7.21e+01	18	901	18	0.2	5631	17	Q91439	Polycystic kidney dis	7.21e+01
829	18	0.2	3751	11	Q24641	Human embryonal kinas	7.21e+01	18	902	18	0.2	5631	24	T08803	Polycystic kidney dis	7.21e+01
830	18	0.2	3757	48	V44332	Murine mmp-6 zymogen	7.21e+01	18	903	18	0.2	5720	25	T42117	Lats gene encoding la	7.21e+01
831	18	0.2	3757	47	V44208	Mouse mast cell prote	7.21e+01	19	904	19	0.2	5830	60	X13218	Enterococcus faecalis	1.97e+01
832	18	0.2	3791	29	T63575	Chicken beta-actin pr	7.21e+01	18	905	18	0.2	5961	16	Q74060	Human interferon-gamm	1.97e+01
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834	18	0.2	3809	2	Q12760	P40 genomic DNA.	7.21e+01	18	907	18	0.2	6169	47	V51368	Human TIGR upstream r	7.21e+01
835	18	0.2	3812	2	Q10091	Partial sequence of m	7.21e+01	18	908	18	0.2	6259	38	T86366	HindIII fragment of P	7.21e+01
836	18	0.2	3821	9	Q56609	Human Pgf-2/Nr-3' 5' f	7.21e+01	18	909	18	0.2	6305	16	Q96127	SM22 protein gene nuc	7.21e+01
837	18	0.2	3830	1	N91260	Nucleotide sequence f	7.21e+01	18	910	18	0.2	6404	7	Q42388	Tobacco leaf antifung	1.97e+01
838	18	0.2	3831	3	Q20262	ERK3.	7.21e+01	18	911	18	0.2	6418	10	Q65395	6.5 kb BanHI fragment	1.97e+01
839	18	0.2	3854	44	V29124	Rattus norvegicus Smo	7.21e+01	18	912	18	0.2	6464	8	Q48770	Osteogenic protein ho	7.21e+01
840	18	0.2	3915	20	T08974	Presumed shortened B-	7.21e+01	18	913	18	0.2	6464	8	Q48772	Arylamine N-acetyl-tr	7.21e+01
841	18	0.2	3919	60	X13618	Enterococcus faecalis	7.21e+01	18	914	18	0.2	6464	8	Q48768	Arylamine N-acetyl-tr	7.21e+01
842	19	0.2	3925	21	T13237	HindIII-BamHI fragmen	1.97e+01	18	915	18	0.2	6568	39	V15949	Nevoid basal cell car	1.97e+01
843	18	0.2	4008	44	V07279	Rat semaphorin W enco	7.21e+01	18	916	18	0.2	6604	60	X13174	Enterococcus faecalis	7.21e+01
844	19	0.2	4027	15	Q90982	Protein p140 cDNA fro	1.97e+01	18	917	18	0.2	6727	37	T88014	Murine IL-5 cDNA geno	1.97e+01
845	19	0.2	4027	15	Q90972	Protein p140 cDNA fro	1.97e+01	18	918	18	0.2	6953	19	T17116	Rhodopsin gene.	7.21e+01
846	18	0.2	4045	60	X13088	Enterococcus faecalis	7.21e+01	18	919	18	0.2	7313	44	V29288	Nucleotide sequence o	7.21e+01
847	19	0.2	4091	1	Q04035	Stem cell leukaemia (1.97e+01	18	920	18	0.2	7623	36	T60556	Plasmid padneo-int us	7.21e+01
848	19	0.2	4102	36	T85575	Human WSX receptor va	1.97e+01	19	921	19	0.2	7920	20	T05899	Human IL-4 gene.	1.97e+01
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850	18	0.2	4126	60	X13277	Enterococcus faecalis	7.21e+01	18	923	18	0.2	7997	15	Q89553	Rat cholesterol 7 alp	1.97e+01
851	19	0.2	4140	1	N92735	Sheep PRP gene for sc	1.97e+01	18	924	18	0.2	7997	15	Q89553	Rat cholesterol 7-alp	7.21e+01
852	18	0.2	4157	51	V45424	Aspergillus oryzae 5-	7.21e+01	18	925	18	0.2	7997	34	T79737	Rat cholesterol 7-alp	7.21e+01
853	18	0.2	4157	40	V19709	5-aminolevulinic acid	7.21e+01	18	926	18	0.2	8045	17	T12237	Retroviral vector WEG	7.21e+01
854	18	0.2	4157	40	V04102	Aspergillus oryzae 5-	7.21e+01	18	927	18	0.2	8174	2	Q13332	GDP-Fuc:beta-D-galact	7.21e+01
855	18	0.2	4180	1	N91773	Rat androgen receptor	7.21e+01	18	928	18	0.2	8174	9	Q56908	DNA encoding a glycos	7.21e+01
856	18	0.2	4192	60	X00725	Human aggrecan degrad	7.21e+01	18	929	18	0.2	8174	29	T61677	Human alpha(1,2)-fuc	7.21e+01
857	19	0.2	4199	1	Q05330	Stem cell leukaemia (1.97e+01	18	930	18	0.2	8388	13	Q78191	Vector M48 used for g	7.21e+01
858	19	0.2	4201	1	N90571	Bovine repeat element	1.97e+01	18	931	18	0.2	9058	41	V10663	Mouse Fas ligand-like	1.97e+01
859	18	0.2	4212	52	V65380	Connective tissue gro	7.21e+01	18	932	18	0.2	9058	41	V10663	Mouse Fas ligand-like	7.21e+01
860	18	0.2	4214	28	T58534	Human connective tiss	7.21e+01	18	933	18	0.2	9096	38	T88015	Human interleukin 16	1.97e+01
861	18	0.2	4221	11	Q64046	A253 derived bcl-1 cd	7.21e+01	18	934	18	0.2	9180	51	V57416	Tumour suppressor gen	1.97e+01
862	18	0.2	4223	44	V22752	Babesia microti BNMI-	7.21e+01	18	935	18	0.2	9299	29	T47716	Mouse bone morphogene	7.21e+01
863	18	0.2	4223	44	V22737	Babesia microti BNMI-	7.21e+01	18	936	18	0.2	9299	29	T47716	Mouse bone morphogene	7.21e+01
864	18	0.2	4232	60	V99328	cDNA encoding a GDNFR	7.21e+01	18	937	18	0.2	9370	13	Q75165	AF-4 transcript (cDNA	7.21e+01
865	18	0.2	4234	57	V080596	Kidney injury associa	7.21e+01	18	938	18	0.2	9391	13	Q75164	AF-4 transcript (cDNA	7.21e+01
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867	18	0.2	4253	34	T86172	Human MLN 51 nucleoti	7.21e+01	18	940	18	0.2	9620	37	T45424	Murine Ataxia-telangi	7.21e+01
868	18	0.2	4253	28	T58361	Tobacco epi-5-ariol	7.21e+01	18	941	18	0.2	9898	42	T20767	Human OCIF genome DNA	1.97e+01
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870	18	0.2	4376	40	V10264	Rat GABA-BR1a recepto	7.21e+01	18	943	18	0.2	10266	22	T33007	Mouse SRY-related gen	7.21e+01
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872	18	0.2	4382	2	Q12759	P40 genomic DNA.	7.21e+01	18	945	18	0.2	10409	47	V42558	Mouse dectin-2 gene.	7.21e+01
873	18	0.2	4438	3	Q14050	Alpha-SI-casein gene.	7.21e+01	18	946	18	0.2	10409	47	V42558	Mouse dectin-2 gene.	7.21e+01
874	18	0.2	4481	1	N90958	Sequence encoding ger	7.21e+01	18	947	18	0.2	10475	2	N80643	Sequence of human pul	7.21e+01
875	18	0.2	4487	3	Q20514	Encodes germ cell alk	7.21e+01	18	948	18	0.2	10475	2	N80643	Genomic clone encodin	7.21e+01
876	19	0.2	4580	41	V06594	Bovine N-proteinase c	1.97e+01	18	949	18	0.2	10597	36	T60554	Plasmid pAGMLVneo-int	7.21e+01
877	18	0.2	4580	37	T32034	Proliferation-inhibit	7.21e+01	18	950	18	0.2	10684	24	T33758	Control region isolat	7.21e+01
878	18	0.2	4595	27	T65123	Human GCAP-1 gene.	7.21e+01	18	951	18	0.2	11236	12	Q70447	Rat nestin gene - its	7.21e+01
879	18	0.2	4668	51	V60918	Angiogenin gene.	7.21e+01	18	952	18	0.2	11288	15	Q90512	CEA clone HindIII-Sau	1.97e+01
880	18	0.2	4722	47	V32836	Rabbit low density li	7.21e+01	18	953	18	0.2	11288	15	Q90512	TGF-beta responsive e	1.97e+01
881	19	0.2	4749	28	T59230	FSP1 promoter linked	1.97e+01	18	954	18	0.2	11298	34	T86756	Human high affinity I	7.21e+01
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884	18	0.2	5009	3	Q21412	Carbonic anhydrase ge	7.21e+01	18	957	18	0.2	12923	3	N90338	Sequence of human mus	7.21e+01
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c 977 18 0.2 18073 59 V83948 Shuttle vector pAdel 7.21e+01
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c 979 18 0.2 22243 58 V74475 Human flavin-containi 1.97e+01
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c 982 18 0.2 26700 59 V81283 Mouse syndecan gene 7.21e+01
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c 984 18 0.2 26700 40 V15426 Mouse poly Ig recepto 7.21e+01
c 985 18 0.2 29392 40 V15426 Calpain large subunit 1.97e+01
c 986 19 0.2 30967 24 T32454 Recombinant adenoviru 7.21e+01
c 987 18 0.2 32026 36 T60559 Recombinant cis-actin 7.21e+01
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c 989 18 0.2 40352 40 V20441 Insert from cosmid 10 1.97e+01
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c 992 18 0.2 53577 28 T18551 Human PKD1 locus betw 7.21e+01
c 993 18 0.2 53577 40 T94108 NC-contig derived fro 7.21e+01
c 994 18 0.2 80240 59 V83940 HC-contig derived fro 7.21e+01
c 995 18 0.2 80595 58 V83939 Hereditary haemochrom 1.97e+01
c 996 19 0.2 235033 51 V57926 Hereditary haemochrom 1.97e+01
c 997 19 0.2 237326 50 V57903

ALIGNMENTS

RESULT 1
ID T38196 standard; DNA; 7653 BP.
AC T38196;
DI 17-DEC-1996 (first entry)
DE Nematode Ced-3 gene.
KW Ced-3; Interleukin-1 beta converting enzyme; ICE; protease;
KW cell death; apoptosis; neural degeneration; inflammation;
KW antinflammatory; ds.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
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FT      23-FEB-1996: U02473.
FT      24-FEB-1995: US-394189.
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FT      PA
FT      Horvitz HR, Shaham S, Yuan J;
FT      WPI; 96-425082/42.
FT      P-PSDB; R98754.
FT      DR
FT      Ced-3 and human interleukin 1-beta convertase genes and proteins
FT      useful to treat inflammation and diseases characterised by cell
FT      death
FT      Claim 18; Fig 3: 139pp; English.
FT      The Caenorhabditis elegans ced-3 gene (T38196) was cloned by
FT      mapping RFLPs and chromosome walking, and genomic DNA cloned
FT      in plasmid pJ107 was sequenced. EMS-induced alleles were also
FT      sequenced. The gene codes for a cell death protein (R98754) that
FT      is structurally similar to human interleukin-1 beta converting
FT      enzyme (ICE) (R98755), suggesting that Ced-3 protein may be a
FT      cysteine protease like ICE and that ICE may be a human equivalent
FT      of the nematode cell death gene. The ced-3 gene can be used as a
FT      probe or in the prodn. of Ced-3 protein and novel drugs for
FT      enhancing or inhibiting the activity of ICE, ced-3 and related
FT      genes for the treatment of inflammatory diseases and/or diseases
FT      caused by cell death. Novel inhibitors of ced-3 activity include
FT      portions of the ced-3 gene and it product.
FT      Sequence 7653 BP; 2429 A; 1456 C; 1270 G; 2498 T;
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Query Match          99.6%; Score 7622; DB 24; Length 7653;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 7652; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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FT FT      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT FT      Horvitz HR, Shaham S, Yuan J;
FT FT      P-PSDB; R45262.
FT FT      Agents which affect activity of cell death genes - used to
FT FT      develop drugs for treating conditions characterised by cell death
FT FT      or proliferation
FT FT      PS
FT FT      Disclosure; Fig 3; 132pp; English.
FT FT      CC
FT FT      This sequence encodes the C.elegans cell death gene, ced-3. Fragments
FT FT      of the amino terminal of the protein encoded by this sequence act as
FT FT      inhibitors of ced-3. This gene has considerable similarity to human
FT FT      interleukin-1beta convertase (ICE), which converts pro-interleukin-
FT FT      1beta to the active cytokine and is involved in inflammatory response
FT FT      in humans. The similarity between the two sequences suggests that
FT FT      inhibitors of ced-3 may also act as inhibitors of ICE. Human ICE and
FT FT      nematode Ced-3 proteins have an overall amino acid similarity of 28%.
FT FT      The ced-3 inhibitors may be used for identifying agents which affect
FT FT      the activity of a gene belonging to the to the ced-3/ICE family of
FT FT      genes and for diagnosis of diseases characterised by cell death. They
FT FT      can also be used to develop drugs for treating conditions characterised
FT FT      by cell deaths such as myocardial infarction, stroke, degenerative
FT FT      disease, traumatic brain injury, hypoxia, pathogenic infection, or
FT FT      hair loss, or drugs for reducing the proliferative capacity or size

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CC of a population of cells such as cancerous cells, cells which produce
CC autoreactive antibodies, infected cells, hair follicle cells or cells
CC which are critical to the life of a parasite, pest or recombinant
CC organism. They may also be used in the diagnosis of inflammatory
CC disease.

SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;

Query Match 96.8%; Score 7405; DB 9; Length 7653;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
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ID Q54666 standard; DNA; 7653 BP.
AC Q54666;
DE 23-JUN-1994 (first entry)
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Key
FH Location/Qualifiers
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FT /rpt_type= INVERTED
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FT FT      /note= "C>T, from alleles n1129 and n1164"
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FT FT      /note= "Inverted w.r.t. repeat 6567-6625"
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FT FT      /tag= aj
FT FT      /number= Exon_8
FT FT      7020
FT FT      /tag= ak
FT FT      /note= "C>T, from allele n1163"
FT FT      W09325685-A.

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PD 23-DEC-1993.
PF 14-JUN-1993; U05701.
PR 12-JUN-1992; US-897788.
PR 20-NOV-1992; US-979638.
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PI Horvitz HR, Shaham S, Yuan J;
DR WPI; 94-007542/01.
DR P-PSDB; R47466.
PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT develop agents to increase or prevent cell death in organisms
PT Claim 2; Fig 4; 127pp; English.
PS This sequence represents the C. elegans ced-3 gene. A 2.8 kb mRNA
CC was identified as the ced-3 transcript and was most abundant in
CC embryos, but was also detected in larvae and young adults, suggesting
CC that ced-3 is expressed not only in cells undergoing cell death. The
CC four largest introns as well as sequences 5' of the start codon
CC contain repetitive elements, some of which have been characterised
CC in non-coding regions of other C. elegans genes, such as fem-1, lin-12
CC and myoD. The Ced-3 protein is 503 amino acids in length. Ced-3 is
CC highly hydrophilic with no significant hydrophobic region that might
CC be a transmembrane region. One region of Ced-3 is very rich in serine.
CC It is thought that this region is involved in protein-protein inter-
CC actions, similar to acid blobs in transcription factors. Of the
CC mutations which occur within the ced-3 gene, eight of the mutations
CC are missense mutations, two are nonsense mutations and two are putative
CC splicing mutations (see also Q64735-45). These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2429 A; 1453 C; 1272 G; 2499 T;

Query Match 94.3%; Score 7219; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7639; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY GTGACAATGGATTCCAGTCTTGGATTCTGTGACGAGGTTCCTGCAATTTCTTCGTCGTG 5880
Db 5881 gatgggacaatcgagagggccattgttcaattttcttgatgtgctgcgcccacaagttc 5940
QY GATGGGACAAATCGAGACGGGCCATTGTTCAAATTTCTGTGATGTGTGCGGCCGCAAGTTC 5940
Db 5941 aggttgaatttatttcttgatgagaataatttcttcaaaaaatctaaaaatagattttt 6000
QY AGGTTGCAATTTAATTTCTTGAATGAGANATATCTCTCAAAAAATCTAANAATAGATTTT 6000

Db 6001 attccgaaaaatcccgatcgaaaaattcgatatataattacgaaaattttgtgataaaatgac 6060
QY ATTCCAGAAATCCCGATCGAAAAATTCGATATAATTAACGAAATTTGTGATAAAATGAC 6060
Db 6061 aaaaacatcacatcgatcgatctccgcccacttcgattggtttgaaagtgggcgga 6120
QY AAACCAATCACATCGTCGATCTCCGCCACTTCATCGGATTTGTTTGAAGTGGCGGA 6120
Db 6121 gtgaattcgtgattggtgcagttttcagtttagaggaatttaaaaatcgccctttcga 6180
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Db 6181 aaattaaaaattgattttttcaattttttgaaaaatatccgattttttattattcttt 6240
QY AAATTAATAAATTTGATTTTTCATTTTTCGAAAAATATTCGGATTTATTTATATTCTTT 6240
Db 6241 ggagcgaagcccgctcctgtaaaacatttttaaatgataataataaatttttgcagcaa 6300
QY GGAGCGAAAGCCCGTCTCTGTAACATTTTAAATGATTAATTAATAATTTTTCGCAAA 6300
Db 6301 gtgtggaaaaagaagccgagccaaagctgaacattctctgattogatacgcacaacagctcaa 6360
QY GTGTGGAAAAAGAGCCGAGCCAAAGCTGACATTCGTATTCGATACGCAACGACAGCTCAA 6360
Db 6361 tatgtttcgtggagaaacagctcgttgatcatcattggttcattcaagcgcgtctggaagt 6420
QY TATGTTTCGTGGAGAAACAGTCTCGTGGATCATGTTGTTTCATTCAGCCGCTGTGGAAGTG 6420
Db 6421 ttctgcacacgcgaagatatgattgttgcgtgctgactgaagtcataaagaag 6480
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Db 6481 gtcgcttgcgatttcagacatcacagggatcgaaatttttagtttttagctaaatgattgttt 6540
QY GTCGCTTGTGGATTTTCAGACATCACAGGGATCGAATATTTTGAACACAGATGCCAGAGGTA 6540
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Db 6721 ccagtaaaaaatctttattagcattgattttactgaaaaacgaaaaattttagtttttc 6780
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QY CCGCCTGCTCAAAAAGTTCTACTTTTGGCGGAGACGAAACTCTGCCGCTCTAAATTC 7080
Db 7081 actcgtgatttcattgccccaaattgataattgctgtatcttctccccagttctcttctg 7140

20-NOV-1992: US-979638.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Shaham S, Yuan J;

DR WPI; 94-007542/01.

DR P-PSDB; R53284.

PT Isolated C elegans cell death genes ced-3 and ced-4 - used to develop agents to increase or prevent cell death in organisms

PS Claim 14; Fig 4; 127pp; English.

CC The sequences given in Q64735-45 represent mutations of the C. elegans ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and was most abundant in embryos, but was also detected in larvae and young adults, suggesting that ced-3 is expressed not only in cells undergoing cell death. The four largest introns as well as sequences 5' of the start codon contain repetitive elements, some of which have been

CC characterised in non-coding regions of other C. elegans genes, such as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in length. Ced-3 is highly hydrophilic with no significant hydrophobic region that might be a transmembrane region. One region of Ced-3 is very rich in serine. It is thought that this region is involved in protein-protein interactions, similar to acid blobs in transcription factors. Of the mutations which occur within the ced-3 gene, eight of the mutations are missense mutations, two are nonsense mutations and two are putative splicing mutations. These mutations establish the null phenotype of the ced-3 gene, confirming that ced-3, like ced-4, function is not essential for viability. The ced-3 and ced-4 gene products may be used to develop agents for treating conditions characterised by cell deaths, such as myocardial infarction, stroke, degenerative disease, traumatic brain injury, hypoxia, pathogenic infection, aging or hair loss.

CC Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;

Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Dbb 1 agatctgaataagtgatgaataataataagtgatgattctcgaggaattgactgt 60

Qy 1 AGATCTGAATAAGGTGATAAATAATAATTAAGTGTATTTCTGAGGAATTTGACTGT 60

Dbb 61 tttagcaataatactgtgttcagaaaaagccagtttctagattttccgtctta 120

Qy 61 TTAGCAATAATACTGTGTTCAGAAAAAGTCCAGTTTCTAGATTTTCCGCTTAA 120

Dbb 121 ttgtcgaataataatccattattacatttttctgctcctcctcgagcgacgtctc 180

Qy 121 TTGTCGAATTAATATCCCTATTATACATTTTTCATGCTCATCTCGAGCGACGTCTC 180

Dbb 181 aaagaattgtgagagcaaacgcgtcccatgacccacactcagcgcccaaacaaac 240

Qy 181 AAAGAATTGTGAGAGCAAAACGCGTCCCATTTGACCTCCACACTAGCGCGCAACAAAC 240

Dbb 241 gtcgaacattcggtgtgtgtccttttccgttatcttgagtcattttgtcgttt 300

Qy 241 GTTCGAACATTCGTGTGTGTGCTCCTTTTCGTTATCTTCAGTCATCTTTTGTGCTTT 300

Dbb 301 tttctttgttctttttgttgacggtgtgtgaagcaattattacatcaattgaagaaaa 360

Qy 301 TTTTCTTTTCTTTTGTGTGAACGTGTGTGAAGCAATTATTACATCAATTGAAGAAAA 360

Dbb 361 gctcgcgatttattgttcagaaaaagattctgagattctcgaagtgatttataata 420

Qy 361 GGCTCGCCGATTATTGTGTCCAGAAAAAGATTCTGAGATTCTCGAAGTGCATTTTATAATA 420

Dbb 421 tttaacctgtgtttgttcattgttctgttaaaaaaaccaactgtttattgtgaaaaacgat 480

Qy 421 TTTAACCTTGGTTTTTGCATTTGTTTGTAAATAAACCACTGTTTATGTGAAAAACCGAT 480

Dbb 481 tagtttactataaaactacttttaaacctttacottttacccgcgcgtcgtgttcgatg 540

Qy 481 TAGTTTTACTTAATAAAACTACTTTTAAACCTTTACCTTTACCTCAGCGCTCCGTTTCATG 540

Dbb 541 gctcatagattttcgtactcaaatcccaataataatttacaggggcaattatgtgaaa 600

Qy 541 TCCGTAATAATTTTCAAGATTTTGGCATTTCCACTTTTAAAGGCGCACAGGATTTATTCCA 600

Qy 541 GCTCATAGATTTTCGATACTCAAAATCCAAAAATAAATTTACGAGGGCAATTAATGTGAAA 600

Dbb 601 caaaaaaacttaagatttccacatgtttgacctctctccggcaccttcttcttcttagcccc 660

Qy 601 CAAAAACAATCCTAAGATTTCACATGTTTGACCTCTCCGGCACCTTCTTCTCTTAGCCCC 660

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Qy 661 ACCACTCCATCACCCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTGAT 720

Dbb 721 ctcatttgatgtctcttctcgatttatagtctcttgcgaatttcaatgcttcaatgctttaa 780

Qy 721 CTCATTGGTATGCTCTTTTCGATTTTAFAGCTCTTTTTCGCAATTTCAATGCTTTAAAC 780

Dbb 781 aatccaaaatcgcatattattgtgcatggaggaacaaatgacggggttggaattcttagatga 840

Qy 781 AATCCAAATCGCATTATATTGTGTCATGGAGCAAAATGACGGGTTTGGAAATCTTAGATGA 840

Dbb 841 gatcaggagcttccagggtaaacgcgcggttcatttttaccacatttccattcttcttcc 900

Qy 841 GATCAGGAGCTTTCAGGGTAAACGCCCGGTTCATTTTGTACCAATTTCAATCAATTTTCT 900

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Qy 901 GTGCTCTTGGTATCTCAACTTGTCCCGGTTTGTCTTCGTCACACTCTTCCGCTGATGC 960

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Qy 961 CACTGTCTCCGTCCTCAATTTATCGTTTAGAAATGTGAATGTGCCAGATGGGTGACTCATA 1020

Dbb 1021 ttgctgctcaaatcaactcttcttctcctcgcgagcttcttcagagcccatcataaac 1080

Qy 1021 TTGCTCTCTCAATTCACATCCACTTTCTTTCTCATCGCGAGTCTTACGAGCCCATCAATAAC 1080

Dbb 1081 tttttttccggaaattgtcaataaacgcggccaaaaactttctccaaattgtttacgcaa 1140

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Dbb 1141 tatatacatccataagaatatcttctcgaattgttatgatttcttcgcgagcactttctct 1200

Qy 1141 TATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTTCTTCGCGACACTTTCTCT 1200

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Qy 1381 AACATTTTGACGCGCAAAATATCTCGTAGCAAAACTACAGTAATTTCTTAAATGACTAC 1440

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Qy 1441 TGTAGCGCTTGTGTCGATTTACGGGCTCAATTTTGAATAATAATTTTTCGAATTT 1500

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Qy 1621 TCCGTAATAATTTTCAAGATTTTGGCATTTCCACTTTTAAAGGCGCACAGGATTTATTCCA 1680

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QY 3901 ATTAATAATACATTTTGTATTTTCAACATCACATGATTAACCCCATATTTTTCGTT 3960
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RESULT 5
ID Q64742 standard; DNA; 7653 BP.
AC Q64742;
DE 23-JUN-1994 (first entry)
DT ced-3 (C6434T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
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FT /note= "Inverted w.r.t. repeat at 1356-1472"
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FT PF 14-JUN-1993; US-897788.
FT PR 12-JUN-1992; US-979638.
FT PR 20-NOV-1992; US-979638.
FT PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT PI Horvitz HR, Shaham S, Yuan J;

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DR WPI: 94-007542/01.
DR P-PSDB: R53285.
DR Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT develop agents to increase or prevent cell death in organisms
PS Claim 14; Fig 4; 127pp; English.
CC The sequences given in Q64735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such
CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations. These mutations establish the
CC two are putative splicing mutations. Confirming that ced-3, like ced-4,
CC null phenotype of the ced-3 gene, confirming that ced-3 and ced-4 gene
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 4981 ggtgtttcaatatgaaatgtattttttaaaaaactttaaaaaaccactccgggaaagcaataa 5040

develop agents to increase or prevent cell death in organisms
 Claim 14: Fig 4: 127bp; English.
 The sequences given in Q64735-45 represent mutations of the C. elegans
 ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
 was most abundant in embryos, but was also detected in larvae and young
 adults, suggesting that ced-3 is expressed not only in cells undergoing
 cell death. The four largest introns as well as sequences 5' of the
 start codon contain repetitive elements, some of which have been
 characterised in non-coding regions of other C. elegans genes, such
 as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
 length. Ced-3 is highly hydrophilic with no significant hydrophobic
 region that might be a transmembrane region. One region of Ced-3 is
 very rich in serine. It is thought that this region is involved in
 protein-protein interactions, similar to acid blobs in transcription
 factors. Of the mutations which occur within the ced-3 gene, eight of
 the mutations are missense mutations, two are nonsense mutations and
 two are putative splicing mutations. These mutations establish the
 null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
 function is not essential for viability. The ced-3 and ced-4 gene
 products may be used to develop agents for treating conditions
 characterised by cell deaths, such as myocardial infarction, stroke,
 degenerative disease, traumatic brain injury, hypoxia, pathogenic
 infection, aging or hair loss.
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FT FT      develop agents to increase or prevent cell death in organisms
FT FT      Claim 14; Fig 4; 127pp; English.
FT FT      The sequences given in Q64735-45 represent mutations of the C. elegans

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CC CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC CC was most abundant in embryos, but was also detected in larvae and young
CC CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC CC cell death. The four largest introns as well as sequences 5' of the
CC CC start codon contain repetitive elements, some of which have been
CC CC characterised in non-coding regions of other C. elegans genes, such
CC CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC CC region that might be a transmembrane region. One region of Ced-3 is
CC CC very rich in serine. It is thought that this region is involved in
CC CC protein-protein interactions, similar to acid blobs in transcription
CC CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC CC the mutations are missense mutations, two are nonsense mutations and
CC CC two are putative splicing mutations. These mutations establish the
CC CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC CC function is not essential for viability. The ced-3 and ced-4 gene
CC CC products may be used to develop agents for treating conditions
CC CC characterised by cell deaths, such as myocardial infarction, stroke,
CC CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC CC infection, aging or hair loss.
CC CC
CC CC Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;
CC CC

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Query Match 93.1%; Score 7126; DB 9; Length 7653;
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RESULT

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ID Q64740 standard; DNA; 7653 BP.
AC Q64740;
DT 23-JUN-1994 (first entry)
DE ced-3 (C6322T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH key Location/Qualifiers
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FT 23-DEC-1993.
FT PD 14-JUN-1993; U05701.
FT PF 12-JUN-1992; US-897788.
FT PR 20-NOV-1992; US-979638.
FT PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT PI Horvitz HR, Shaham S, Yuan J;
FT WP1; 94-007542/01.
FT P-PSDB; R53283
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT Claim 14; Fig 4; 127pp; English.
FT PS The sequences given in Q64735-45 represent mutations of the C. elegans
FT CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT CC was most abundant in embryos, but was also detected in larvae and young
FT CC adults, suggesting that ced-3 is expressed not only in cells undergoing
```


CC cell death. The four largest introns as well as sequences 5' of the
 CC start codon contain repetitive elements, some of which have been
 CC characterised in non-coding regions of other *C. elegans* genes, such
 CC as fem-1, lin-12 and myoB. The Ced-3 protein is 503 amino acids in
 CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
 CC region that might be a transmembrane region. One region of Ced-3 is
 CC very rich in serine. It is thought that this region is involved in
 CC protein-protein interactions, similar to acid blobs in transcription
 CC factors. Of the mutations which occur within the ced-3 gene, eight of
 CC the mutations are missense mutations, two are nonsense mutations and
 CC two are putative splicing mutations. These mutations establish the
 CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
 CC function is not essential for viability. The ced-3 and ced-4 gene
 CC products may be used to develop agents for treating conditions
 CC characterised by cell deaths, such as myocardial infarction, stroke,
 CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
 CC infection, aging or hair loss.

SO Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;
 Query Match 93.18; Score 7126; DB 9; Length 7653;
 Best Local Similarity 99.84; Pred. No. 0.00e+00;
 Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT Claim 14; Fig 4; 127pp; English.
FT
FT The sequences given in 064735-45 represent mutations of the C. elegans
FT ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT was most abundant in embryos, but was also detected in larvae and young
FT adults, suggesting that ced-3 is expressed not only in cells undergoing
FT cell death. The four largest introns as well as sequences 5' of the
FT start codon contain repetitive elements, some of which have been
FT characterised in non-coding regions of other C. elegans genes, such

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CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
CC
CC Query Match          93.1%; Score 7126; DB 9; Length 7653;
CC Best Local Similarity 99.8%; Pred. No. 0.00e+00;
CC Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP: 2429 A; 1452 C; 1272 G; 2500 T;

Query Match 93.18; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.84; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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 12-JUN-1992; US-897788.
 20-NOV-1992; US-979638.
 (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PI Horvitz HR, Shaham S, Yuan J;
 WPI: 94-007542/01.
 P-PSDB; R53280.
 Isolated C elegans cell death genes ced-3 and ced-4 - used to develop agents to increase or prevent cell death in organisms Claim 14; Fig 4; 127pp; English.
 The sequences given in Q64735-45 represent mutations of the C. elegans ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and was most abundant in embryos, but was also detected in larvae and young adults, suggesting that ced-3 is expressed not only in cells undergoing cell death. The four largest introns as well as sequences 5' of the start codon contain repetitive elements, some of which have been characterised in non-coding regions of other C. elegans genes, such as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in length. Ced-3 is highly hydrophilic with no significant hydrophobic region that might be a transmembrane region. One region of Ced-3 is very rich in serine. It is thought that this region is involved in protein-protein interactions, similar to acid blobs in transcription factors. Of the mutations which occur within the ced-3 gene, the following

CC the mutations are missense mutations, two are nonsense mutations and two are putative splicing mutations. These mutations establish the CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4, CC function is not essential for viability. The ced-3 and ced-4 gene CC products may be used to develop agents for treating conditions CC characterised by cell deaths, such as myocardial infarction, stroke, CC degenerative disease, traumatic brain injury, hypoxia, pathogenic CC infection, aging or hair loss.
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Qy 5221 ACAGCTTCGAGAGTTTGAATTTACAGTACTCCTTAAGGCGCACACCCCATTTGCGATGG 5280
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CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP: 2430 A; 1453 C; 1271 G; 2499 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy 1 AGATCGAATAAGGTGATATAATAATTAAGTGTATTCTGAGGAAATTTGACTGT 60
Db 61 tttagcagaattaattctgtttcagaaaaaagtcaggtttcttagattttccggtcta 120
Qy 61 TTTAGCACAAATTAATCTGTGTTTCAGAAAAAAGTCAGGTTTCTAGATTTTTCCGCTTA 120
Db 121 tttagcagaattaattctgtttcagaaaaaagtcaggtttcttagattttccggtcta 180
Qy 121 TTTGTCGAATTAATCCCTAATATCACTTTTTCATGCTCATCTCGAGCGGCACGTCCTC 180
Db 181 aaagaattgagagcaaacgcgcctccattgacctccacactcagccgcacaaacaaac 240
Qy 181 AAGAAATGTGAGAGCAAAAGCGCGCTCCCAATGACCTCCACATCAGCCGCCAAACAAAC 240
Db 241 gttcgaacattcgt 300
Qy 241 GTTCGAACATTCGT 300
Db 301 tttctgt 360
Qy 301 TTTTCTGT 360
Db 361 ggtcgcgaatttatgtgacgaagaattctgagattctgagattctgagattctgagatt 420
Qy 361 GGCTCGCGGATTATGTTGCCAGAAAGATCTGAGATCTCGAAGTCGATTTTAAATA 420
Db 421 tttaacctgt 480
Qy 421 TTTAACTGT 480
Db 481 tagtttactataaaactacttttaaacctttacaccttaacctcaacctgtgtgtgtgtgt 540
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Qy 1441 TGTAGCGCTGT 1500
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FT 23-DEC-1993.
FT 14-JUN-1993. U05701.
FT 12-JUN-1992; US-897788.
FT 20-NOV-1992; US-979638.
FT (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT Horvitz HR, Shaham S, Yuan J;
FT WPI: 94-007542/01.
FT P-PSDB: R53282.
FT
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT Claim 14; Fig 4; 127pp; English.
FT
FT The sequences given in Q64735-45 represent mutations of the C. elegans
FT ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT was most abundant in embryos, but was also detected in larvae and young
FT adults, suggesting that ced-3 is expressed not only in cells undergoing
FT cell death. The four largest introns as well as sequences 5' of the
FT start codon contain repetitive elements, some of which have been
FT characterised in non-coding regions of other C. elegans genes, such
FT as fem-1, lin-12 and myoD. The ced-3 protein is 503 amino acids in
FT length. Ced-3 is highly hydrophilic with no significant hydrophobic
FT region that might be a transmembrane region. One region of Ced-3 is
FT very rich in serine. It is thought that this region is involved in
FT protein-protein interactions, similar to acid blobs in transcription
FT factors. Of the mutations which occur within the ced-3 gene, eight of
FT the mutations are missense mutations, two are nonsense mutations and
FT two are putative splicing mutations. These mutations establish the
FT null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
FT function is not essential for viability. The ced-3 and ced-4 gene
FT products may be used to develop agents for treating conditions
FT characterised by cell deaths, such as myocardial infarction, stroke,
FT degenerative disease, traumatic brain injury, hypoxia, pathogenic
```

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CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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RESULT 14
ID Q79970 standard; cdna; 2485 BP.
AC Q79970;
DE 13-SEP-1995 (first entry)
DT Interleukin-1 beta converting enzyme homolog ced3 cdna.
KW Interleukin-1 beta converting enzyme; homolog ced3;
KW oncogene bcl-2; programmed cell death; cancer treatment; ss.
OS Caenorhabditis elegans.
FH Key
FT Location/Qualifiers
FT cds
FT 17..1528
FT /*tag= a
FT W09500160-A.
PN 05-JAN-1995.
PD 10-JUN-1994; U06630.
PF 24-JUN-1993; US-080850.
PR (GEO) GEN HOSPITAL CORP.
PA Miura M, Yuan J;
PI WPI; 95-051742/07.
DR P-PSDB; R66770.
PT Promoting or preventing programmed cell death in vertebrate cells
PT - by inhibiting the activity of interleukin-1 beta converting
PT enzyme.
PS Example 1; Fig 2C; 116pp; English.
CC Q79970 encodes R66770 interleukin-1 beta converting enzyme homolog
CC ced3, increasing ced3s enzymatic activity can promote the
CC programmed cell death of cancer cells (pref. those overexpressing
CC the bcl-2 oncogene), this can be used as the basis of a new cancer
CC treatment. Alternatively by reducing ced3s enzymatic activity
CC programmed cell death can be inhibited, this may be useful in the
CC development of new cell lines which remain viable in culture for
CC extended or indefinite periods, independent of growth factors.
CC Sequence 2485 BP; 564 A; 564 G; 480 G; 757 T;
SQ
Query Match 6.68; Score 505; DB 14; Length 2485;
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Db 1884 tcgattaatatttaacctatttttttcgccccaaaaaaatcttaataattgaattacgaatag 1943
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QY 7431 TCGATTAAATTTAACTATTATTTTCGCCACAAAAAATCTAATATTGATTAAACGAATAG 7490
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QY 7491 CATTCCCATCTCTCCCGTCCGGAA 7515
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RESULT 15

ID Q54629 standard; DNA; 6560 BP.
AC Q54629;
DE 23-JUN-1994 (first entry)
DT Genomic region containing ced-9 gene.
KW Cell death; senescence; programmed cell death; ced-9; myocardial
KW infarction; stroke; brain injury; neurodegenerative disease;
KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
KW oncogene; ss.
OS Caenorhabditis elegans.
PN W09325683-A.
PD 23-DEC-1993.
PF 14-JUN-1993; U05651.
PR 12-JUN-1992; US-898933.
PR 10-AUG-1992; US-927681.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Hengartner M, Horvitz HR;
DR WPI; 94-007540/01.
PT Caenorhabditis elegans cell death-protective gene - used to
PT develop agents for preventing cell death or for reducing
PT population of cells
PS Claim 3; Page 54-58; 112pp; English.
CC ced-9 is essential for C. elegans development and apparently
CC functions by protecting cells during development from programmed
CC cell death. ced-9 was shown to function by antagonising the
CC activities of cell death genes ced-3 and ced-4. The protein product
CC of the human oncogene bcl-2 was found to have a similar sequence
CC to the ced-9 protein. The ced-9 gene can be used for developing
CC agents for treating a condition characterised by increased cell death
CC such as myocardial infarction, stroke, traumatic brain injury,
CC neurodegenerative disease, muscular degenerative disease, ageing,
CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
CC be used for reducing a population of cells in the treatment of
CC neoplastic growth cancerous tissue, infected cells or autoreactive
CC immune cells.
SQ Sequence 6560 BP; 2040 A; 1274 C; 1203 G; 2023 T;

Query Match 0.5%; Score 39; DB 9; Length 6560;
Best Local Similarity 100.0%; Pred. No. 1.18e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cp 1435 CATTTAAGAATTACTGTAGTTTCGCTACGAGATATTT 1397
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93	20	0.3	290	24	AA680971	LnFrAm0589 Leishmania	1.19e-01	166	20	0.3	349	27	AI462927	v1806G08.x1 Soares mous	1.19e-01
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95	20	0.3	291	20	AA902486	OK91G08.s1 NCI_CGAP_Lu	1.19e-01	168	21	0.3	350	22	AI030268	qB28E10.x1 Soares_breg	6.31e-03
96	21	0.3	293	27	AA958318	UI-R-C0-ia-c-08-0-UI.s	6.31e-03	169	20	0.3	353	35	D44824	HMSUP1276 Human brain	1.19e-01
97	20	0.3	294	32	H87782	Y575d08.s1 Soares reti	1.19e-01	170	21	0.3	353	38	B94008	CIT-HSP-2168J22.TF CIT	6.31e-03
98	20	0.3	295	37	FR0011335	F.rubripes GSS sequenc	1.19e-01	171	21	0.3	354	33	W03051	ma69H08.r1 Soares mous	6.31e-03
99	20	0.3	299	36	C21893	C21893 Valencia orange	1.19e-01	172	21	0.3	354	25	AI322082	HS_3242.B2_G07.T7 CIT	6.31e-03
100	21	0.3	299	13	AA57251	aa91e05.s1 Stratagene	6.31e-03	173	21	0.3	354	39	AQ220375	UT-R-A0-ak-e-10-0-UI.s	1.19e-01
101	21	0.3	300	39	AQ100181	HS_3049.B2_F10 MR CIT	6.31e-03	174	20	0.3	355	26	AA859059	HS_3242.B2_G07.T7 CIT	6.31e-03
102	20	0.3	300	15	C29898	C29898 Yuji Kohara unp	1.19e-01	175	20	0.3	355	38	AQ027225	CIT-HSP-2371F21.TF CIT	1.19e-01
103	26	0.3	300	15	C32017	C32017 Yuji Kohara unp	1.19e-01	176	20	0.3	356	34	W69992	CIT-HSP-2314J13.TF CIT	1.19e-01
104	26	0.3	300	15	C37964	C37964 Yuji Kohara unp	1.19e-01	177	22	0.3	357	15	AI1501	zD51a10.r1 Soares_feta	1.19e-01
105	24	0.3	300	15	C52036	C52036 Yuji Kohara unp	1.19e-01	178	20	0.3	357	39	AQ112823	CIT-HSP-2371F21.TF CIT	1.19e-01
106	20	0.3	300	15	C34591	C34591 Yuji Kohara unp	1.19e-01	179	20	0.3	357	39	AI1501	CIT-HSP-2371F21.TF CIT	1.19e-01
107	20	0.3	300	41	AQ316539	CIT-HSP-2384L16.TPB CI	1.19e-01	180	20	0.3	357	32	H83932	Y564C04.s1 Soares reti	1.19e-01
108	20	0.3	301	27	AA957697	UI-R-EL-fw-g-03-0-UI.s	1.19e-01	181	20	0.3	357	32	H83932	Y564C04.s1 Soares reti	1.19e-01
109	20	0.3	303	12	AA379146	EST92195 Skin tumor i	1.19e-01	182	20	0.3	358	40	AQ265549	RPC111-76C24.TJ RPC111	1.19e-01
110	23	0.3	304	26	AA399740	h2h8H05.x1 NCI_CGAP_Fr	1.17e-05	183	21	0.3	359	8	T00037	WEST00758 Early embryo	6.31e-03
111	20	0.3	304	26	AA399740	h2h8H05.x1 NCI_CGAP_Fr	1.17e-05	184	21	0.3	359	8	T00037	WEST00758 Early embryo	6.31e-03
112	23	0.3	304	24	AU034595	AU034595 Dictyostellium	1.19e-01	185	20	0.3	360	15	C50455	C50455 Yuji Kohara unp	2.90e-04
113	20	0.3	304	24	AI248368	qh76a10.x1 Soares_feta	1.17e-05	186	22	0.3	360	15	C64964	C64964 Yuji Kohara unp	2.90e-04
114	20	0.3	306	30	R46062	yq47h06.s1 Soares inf	1.19e-01	187	22	0.3	360	32	D67664	CELK076C9F Yuji Kohara	2.90e-04
115	20	0.3	307	24	AI225900	ui23b06.y1 Soares mous	1.19e-01	188	21	0.3	360	15	C62642	C62642 Yuji Kohara unp	2.90e-04
116	20	0.3	309	37	FR0028277	Fugu rubripes GSS sequ	1.19e-01	189	21	0.3	360	32	D70188	CELK100C2F Yuji Kohara	6.31e-03
117	20	0.3	310	10	AA937749	EST113320 Infant brain	1.19e-01	190	20	0.3	360	32	D70188	CELK100C2F Yuji Kohara	6.31e-03
118	24	0.3	311	8	T03201	qu84a05.x1 NCI_CGAP_Ga	1.19e-01	191	20	0.3	360	19	F06515	HSC1AG041 normalized i	1.19e-01
119	20	0.3	314	15	AA608686	ae55g12.s1 Stratagene	1.19e-01	192	20	0.3	360	15	C68005	Y564C04.s1 Soares reti	1.19e-01
120	20	0.3	314	39	B86304	RPC111-22K17.TV RPC111	1.19e-01	193	20	0.3	361	31	H56539	Y564C04.s1 Soares reti	1.19e-01
121	21	0.3	315	33	Y11688	mb17b06.r1 Soares mous	6.31e-03	194	21	0.3	362	39	B89390	RPC111-27G9.TPB RPI	1.19e-01
122	20	0.3	315	17	AA741717	LnLW39P3/349B Leishman	1.19e-01	195	21	0.3	362	39	B89390	RPC111-27G9.TPB RPI	1.19e-01
123	20	0.3	316	38	B70969	CIT-HSP-2063H12.TR CIT	1.19e-01	196	21	0.3	362	23	AI175024	EST218542 Normalized r	6.31e-03
124	20	0.3	317	12	AI348720	EST55215 Hippocampus I	1.19e-01	197	21	0.3	362	20	C84227	C84227 Dictyostellium d	6.31e-03
125	21	0.3	317	28	AI508356	vx46g11.y1 Stratagene	6.31e-03	198	20	0.3	363	21	AA085341	am79H05.s1 Stratagene	6.31e-03
126	20	0.3	317	19	R21668	Y950a12.r1 Soares inf	1.19e-01	199	20	0.3	365	22	AI100430	HS_2268.A1_C05 MF CIT	1.19e-01
127	20	0.3	319	16	AA647096	vn39f05.r1 Stratagene	1.19e-01	200	20	0.3	366	27	AI440044	34805 Lambda-PRL2 Arab	1.19e-01
128	20	0.3	319	35	C14190	C14190 Clontech human	1.19e-01	201	20	0.3	367	34	W52069	zC47d12.r1 Soares_sene	1.19e-01
129	20	0.3	320	35	AQ100859	HS_3060.AL_E03 MR CIT	1.19e-01	202	20	0.3	369	12	AA389959	vb30a04.r1 Soares mous	1.19e-01
130	20	0.3	320	35	AQ063349	zm04b09.s1 Stratagene	1.19e-01	203	20	0.3	369	26	AA389959	UI-R-A0-bh-f-09-0-UI.s	1.19e-01
131	20	0.3	321	37	FR0006855	F.rubripes GSS sequenc	1.19e-01	204	20	0.3	369	8	T02008	WEST02729 Early embryo	1.19e-01
132	20	0.3	321	34	AA001364	zh82d06.r1 Soares_feta	1.19e-01	205	20	0.3	371	41	AQ358917	HS_5021.B2_G09.SP6E RP	1.19e-01
133	20	0.3	321	36	AA093001	ml825.seq.F Human feta	1.19e-01	206	20	0.3	371	39	AQ212127	HS_3241.B1_G07 MR CIT	1.19e-01
134	21	0.3	324	35	AQ027751	ml15b12.r1 Soares mous	6.31e-03	207	20	0.3	372	33	N97723	1151C3 czapFDd2.1, De	1.19e-01
135	20	0.3	324	37	B43947	ml15b12.r1 Soares mous	6.31e-03	208	21	0.3	372	28	AI551615	ve37e07.y1 Soares mous	6.31e-03
136	21	0.3	325	39	AQ089851	HS-1058-B1-D01-MF.abi	1.19e-01	209	21	0.3	373	28	B40243	HS-1051-A1-G03-MF.abi	6.31e-03
137	21	0.3	328	25	AQ000974	AT000974 Bombyx mandar	6.31e-03	210	21	0.3	374	25	AU038621	AU038621 Dictyostellium	6.31e-03
138	20	0.3	330	32	H84763	Ys70e02.r1 Soares reti	1.19e-01	211	21	0.3	374	37	FR0034383	Fugu rubripes GSS sequ	6.31e-03
139	20	0.3	330	24	AU034903	AU034903 Dictyostellium	1.19e-01	212	20	0.3	374	39	AQ084961	HS_2265.B2_E03 MF CIT	1.19e-01
140	20	0.3	334	20	AA855840	w775e09.r1 Stratagene	1.19e-01	213	20	0.3	374	41	AQ356265	CITBI-EL-2529D12.TR CI	1.19e-01
141	20	0.3	337	28	AA559913	h2h7d09.x1 Soares_NNHH	1.19e-01	214	20	0.3	374	39	AQ135849	CIT-HSP-2357114.TR CIT	1.19e-01
142	20	0.3	337	38	AQ047247	RPC111-36A1.TK RPC111	1.19e-01	215	20	0.3	377	15	C68758	HS_3064.A2_H06 MR CIT	1.19e-01
143	22	0.3	338	9	AA163390	ms66b10.r1 Stratagene	2.90e-04	216	20	0.3	377	39	AQ135849	C68758 Yuji Kohara unp	1.19e-01
144	20	0.3	338	15	C75167	C75167 Human pancreati	1.19e-01	217	21	0.3	378	21	AQ103968	HS_3107.AL_D10.T7 CIT	1.19e-01
145	20	0.3	338	32	H84778	Ys71f05.s1 Soares reti	1.19e-01	218	20	0.3	378	40	AQ275485	UB04g04.r1 Soares mous	6.31e-03
146	22	0.3	339	12	AA396639	Yb23d09.r1 Soares mous	2.90e-04	219	20	0.3	379	27	AI470580	RPC1-1-107N1SP6 RPI-1	1.19e-01
147	21	0.3	339	25	AA308423	AU038423 Dictyostellium	6.31e-03	220	20	0.3	380	38	AQ061897	t192a05.x1 NCI_CGAP_X1	1.19e-01
148	20	0.3	340	10	AA256396	zr85g04.s1 Soares_NNHH	1.19e-01	221	20	0.3	380	37	FR0019521	CIT-HSP-2357114.TR CIT	1.19e-01
149	20	0.3	340	37	FR0032336	Fugu rubripes GSS sequ	1.19e-01	222	20	0.3	380	23	AI146206	UI-R-EL-fa-c-04-0-UI.s	1.19e-01
150	20	0.3	342	30	H01895	Yj32f09.s1 Soares plac	1.19e-01	223	21	0.3	381	18	AA797405	w27e09.r1 Soares mous	6.31e-03
151	22	0.3	342	11	AA311800	EST182536 Jurkat T-cel	2.90e-04	224	20	0.3	382	31	AA5019	yo40h06.r1 Soares adu1	1.19e-01
152	21	0.3	345	21	AA959845	W54h11.s1 Soares mous	2.90e-04	225	20	0.3	382	11	AA324362	EST21713 Cerebellum II	1.19e-01
153	21	0.3	345	33	N75835	za96b10.s1 Soares_feta	6.31e-03	226	20	0.3	383	36	AA114906	z104e10.s1 Soares_preg	1.19e-01
154	20	0.3	345	38	B85569	RPC111-20A16.TV RPC111	1.19e-01	227	20	0.3	383	39	AQ204831	HS_3230.B1_E11 MR CIT	1.19e-01
155	20	0.3	345	9	AA200899	mul6f11.r1 Soares 2Nbm	1.19e-01	228	20	0.3	383	15	AA584948	nn41b09.s1 NCI_CGAP_GC	1.19e-01
156	20	0.3	345	32	H80030	Ys65h10.s1 Soares reti	1.19e-01	229	20	0.3	384	22	AU018402	AU018402 Mouse eight-c	1.19e-01

230	0.3	385 39	AF046559	Mus musculus clone OST	1.19e-01	c 303	20	0.3	430 24	AI267578	ag91c10.x1 Stanley Fro	1.19e-01
231	0.3	385 38	AQ024535	HS_218B_A2_C10_MF CIT	1.19e-01	c 304	20	0.3	430 30	R80668	Yi93g03.s1 Soares plac	1.19e-01
232	0.3	386 42	AQ426805	CITBI-E1-2572D17.TF CIT	6.31e-03	c 305	20	0.3	431 13	AA421391	zuo6f01.r1 Soares test	1.19e-01
233	0.3	386 24	A1244286	qj81c03.x1 NCI_CGAP_Ki	1.19e-01	c 306	20	0.3	431 40	B80364	CIT-HSP-2045I11.TR CIT	1.19e-01
234	0.3	387 23	AI154723	oe36g10.r1 Soares mous	6.31e-03	c 307	20	0.3	432 20	AA865636	Q89a03.s1 NCI_CGAP_Ki	1.19e-01
235	0.3	390 18	AA825855	ue23a11.s1 NCI_CGAP_Br	6.31e-03	c 308	20	0.3	432 42	AQ429586	CITBI-E1-2560B16.TR CIT	1.19e-01
236	0.3	391 38	AQ014727	HS_2176_A2_H03_MF CIT	6.31e-03	c 309	20	0.3	432 23	AI182075	ud75g05.x1 Sugano mous	1.19e-01
237	0.3	391 9	AQ206148	zq33d04.r1 Stratagene	1.19e-01	c 310	20	0.3	432 32	N26664	Yx93c06.s1 Soares mela	1.19e-01
238	0.3	393 38	B82386	RPC111-15C4.TPB RPC111	1.19e-01	c 311	21	0.3	433 18	C86443	C86443 Mouse fertilize	6.31e-03
239	0.3	393 22	AI083112	TENU3789 T. cruzi epim	1.19e-01	c 312	20	0.3	433 20	AQ039802	mu33d02.r1 Soares 2NDM	1.19e-01
240	0.3	394 39	AQ132969	HS_2164_A2_G05_MF CIT	1.19e-01	c 313	20	0.3	433 9	AA200384	UI-R-CO-jj-e-03-0-UI.s	1.19e-01
241	0.3	395 40	AI017143	HS_3073_B2_H08_MR CIT	6.31e-03	c 314	20	0.3	433 22	AI043814	UI-R-CO-jj-e-03-0-UI.s	1.19e-01
242	0.3	395 19	T99983	Yx69b12.r1 Soares feta	4.19e-07	c 315	20	0.3	434 18	AA821048	Yz74c09.s1 Soares_mult	1.19e-01
243	0.3	395 42	AQ433327	HS_5123_B2_C11_SF6E.RP	1.19e-01	c 316	20	0.3	434 33	N58835	Yz74c09.s1 Soares_mult	1.19e-01
244	0.3	395 27	AI494931	mp93c05.x1 Soares 2NDM	1.19e-01	c 317	21	0.3	434 25	AI291489	q79b12.x1 Soares_feta	6.31e-03
245	0.3	396 21	AA973487	co45d11.s1 NCI_CGAP_Lu	1.19e-01	c 318	20	0.3	434 34	W67412	z4d0g02.r1 Soares_feta	1.19e-01
246	0.3	397 10	AA265655	mw14e11.r1 Soares mous	1.19e-01	c 319	21	0.3	435 39	AQ113289	CIT-HSP-2379N23.TF CIT	6.31e-03
247	0.3	398 39	AQ129875	HS_2252_A2_B06_MF CIT	1.19e-01	c 320	20	0.3	435 37	FR0006850	F.rubripes GSS sequenc	1.19e-01
248	0.3	398 39	AQ129808	HS_3028_B2_C10_MR CIT	1.19e-01	c 321	21	0.3	436 13	AA462929	Yf92a04.r1 Soares mous	6.31e-03
249	0.3	398 41	AQ346699	RPC111-124C13.IU RPC11	1.19e-01	c 322	20	0.3	437 37	FR0017254	F.rubripes GSS sequenc	1.19e-01
250	0.3	399 28	AI550327	vx07g04.x1 Soares 2NDM	6.31e-03	c 323	20	0.3	437 37	FR0008122	F.rubripes GSS sequenc	1.19e-01
251	0.3	399 39	AQ106570	HS_3082_B1_D12_MF CIT	6.31e-03	c 324	20	0.3	438 38	AQ017741	CIT-HSP-2304A5.TF CIT	1.19e-01
252	0.3	399 33	W32674	zc70c02.s1 Soares_feta	1.19e-01	c 325	22	0.3	439 14	C24568	C24568 Dictyostelium d	2.90e-04
253	0.3	399 37	FR0027107	F.rubripes GSS sequenc	1.19e-01	c 326	21	0.3	439 41	AQ350324	RPC111-133D2.TV RPC111	6.31e-03
254	0.3	400 26	AI381631	te41b07.x1 Soares_NHM	1.19e-01	c 327	20	0.3	440 18	AA805038	nv97e05.s1 NCI_CGAP_Pr	1.19e-01
255	0.3	400 40	AQ153142	HS_2221_A1_F04_MF CIT	1.19e-01	c 328	20	0.3	441 35	AA063067	z4f6e03.s1 Soares_pine	1.19e-01
256	0.3	401 21	AA989917	ua51b10.r1 Stratagene	1.19e-01	c 329	20	0.3	442 30	AA09638	Yf92a06.s1 Soares mela	1.19e-01
257	0.3	401 12	AA398554	te77e03.s1 Soares test	1.19e-01	c 330	20	0.3	442 9	AA218147	mv61f01.r1 Soares mous	1.19e-01
258	0.3	402 37	FR0023961	F.rubripes GSS sequenc	1.19e-01	c 331	20	0.3	442 28	AI535195	UI-R-C3-ta-c-01-0-UI.s	1.19e-01
259	0.3	404 22	A1047230	uh63a10.r1 Soares mous	6.31e-03	c 332	20	0.3	442 41	AQ286478	RPC111-78H1.TJ RPC111	1.19e-01
260	0.3	404 38	AQ006091	CIT-HSP-2288L13.TF CIT	1.19e-01	c 333	20	0.3	443 26	AI356342	qz26c12.x1 NCI_CGAP_GL	1.19e-01
261	0.3	405 37	FR0019324	F.rubripes GSS sequenc	6.31e-03	c 334	20	0.3	445 39	AQ94791	RPC111-60C2.TK RPC111	1.19e-01
262	0.3	406 18	AA828873	cd74g06.s1 NCI_CGAP_Ov	6.31e-03	c 335	20	0.3	445 38	B93391	CIT-HSP-2172D11.TR CIT	1.19e-01
263	0.3	406 28	AI497574	fbg3d03.x1 Zebrafish W	6.31e-03	c 336	20	0.3	446 10	AA276120	vc28a01.r1 Barstead MP	1.19e-01
264	0.3	406 22	AU015111	AU015111 Mouse two-cel	1.19e-01	c 337	20	0.3	446 28	AI504793	v11e02.x1 Stratagene	1.19e-01
265	0.3	406 22	AU015110	AU015110 Mouse two-cel	1.19e-01	c 338	20	0.3	446 22	AI077135	TENU3283 T. cruzi epim	1.19e-01
266	0.3	407 13	AA449432	zx05c06.s1 Soares tota	1.19e-01	c 339	20	0.3	447 24	AU034051	AU034051 Dictyostelium	1.19e-01
267	0.3	407 32	H66656	Yr77e12.s1 Soares_feta	1.19e-01	c 340	20	0.3	447 28	AI551337	vx45d09.x1 Stratagene	1.19e-01
268	0.3	407 39	AQ088651	HS_2208_B1_G09_MR CIT	1.19e-01	c 341	22	0.3	448 34	Z74652	MMTC2 Mouse brain ATC	2.90e-04
269	0.3	408 25	A1341621	qq95a05.x1 Soares tota	1.19e-01	c 342	20	0.3	448 39	AQ136810	HS_2213_A2_D12_MR CIT	1.19e-01
270	0.3	410 21	AA968214	uh4f04.r1 Soares mous	1.19e-01	c 343	21	0.3	448 27	FR0028939	UI-R-CO-10-b-09-0-UI.s	6.31e-03
271	0.3	410 21	AA986516	ue44c05.x1 Sugano mous	1.19e-01	c 344	20	0.3	448 37	FR0008798	F.rubripes GSS sequenc	1.19e-01
272	0.3	411 39	AI115654	RPC111-50M15.TK RPC111	1.19e-01	c 345	20	0.3	449 15	AA605777	fa19c12.s1 Ekkerarly	1.19e-01
273	0.3	412 41	AQ351741	CITBI-E1-254K19.TF CI	1.19e-01	c 346	20	0.3	449 13	AA423723	EST18621 Cerebellum II	1.19e-01
274	0.3	413 42	AQ423645	CITBI-E1-2563N20.TF CI	6.31e-03	c 347	20	0.3	450 13	AA427766	zw49b01.r1 Soares tota	1.19e-01
275	0.3	413 40	AQ154128	HS_3219_A1_E01_MR CIT	1.19e-01	c 348	20	0.3	450 14	AA524335	ng34h02.s1 NCI_CGAP-Co	1.19e-01
276	0.3	414 23	AI175137	EST12859 Normalized r	6.31e-03	c 349	22	0.3	451 40	AQ178604	HS_2242_B1_G09_MR CIT	2.90e-04
277	0.3	414 25	AI317550	uk60f07.Y1 Schiller mo	1.19e-01	c 350	21	0.3	451 20	AA914896	vy95h07.r1 Soares mous	6.31e-03
278	0.3	414 14	AA560374	vl39d08.r1 Stratagene	1.19e-01	c 351	20	0.3	451 16	AA680233	ac82h02.s1 Stratagene	1.19e-01
279	0.3	415 13	AA414165	vc59c07.s1 Knowles Sol	6.31e-03	c 352	20	0.3	451 25	AI342645	qt35g12.x1 Soares_preg	1.19e-01
280	0.3	415 35	AA063510	zif70e04.r1 Soares_pine	1.19e-01	c 353	22	0.3	451 26	AI381944	te72g04.x1 Soares_NFL	2.90e-04
281	0.3	415 40	AQ154128	HS_2164_A2_G01_MR CIT	1.19e-01	c 354	20	0.3	452 33	W02720	zc65b08.s1 Soares_feta	1.19e-01
282	0.3	417 13	AA423127	ve37e07.r1 Soares mous	6.31e-03	c 355	20	0.3	452 36	AA819768	UI-R-A0-av-h-09-0-UI.s	1.19e-01
283	0.3	418 9	AA168686	ms33f06.r1 Stratagene	1.19e-01	c 356	20	0.3	453 25	C06804	C06804 Rat pancreatic	1.19e-01
284	0.3	418 23	AI112513	UI-R-YO-mg-e-09-0-UI.s	1.19e-01	c 357	20	0.3	454 40	AQ339288	RPC111-71J1.TK RPC111	1.19e-01
285	0.3	418 23	AI172037	EST128032 Normalized r	1.19e-01	c 358	20	0.3	454 31	H49126	Yc21e08.r1 Soares adul	1.19e-01
286	0.3	420 18	AA789526	wvl2d09.r1 Soares 2NDM	6.31e-03	c 359	20	0.3	455 40	AQ427779	HS_2063_A2_E06_MR CIT	1.19e-01
287	0.3	421 37	AQ011884	HS_2172_B1_MR_B06 CIT	1.19e-01	c 360	20	0.3	456 30	R66226	Yi34b06.r1 Soares plac	1.19e-01
288	0.3	421 26	AA955067	UI-R-A1-ev-g-11-0-UI.s	1.19e-01	c 361	20	0.3	457 37	BI5718	34595.TV CIT978SKAI Ho	1.19e-01
289	0.3	422 24	AI194454	ue77b05.r1 Soares mous	1.19e-01	c 362	20	0.3	458 27	AI426905	mn01e02.x1 Stratagene	1.19e-01
290	0.3	422 23	AI181207	ub82c11.r1 Soares 2NDM	1.19e-01	c 363	20	0.3	458 40	AQ183933	HS_3226_AL_G11_MR CIT	1.19e-01
291	0.3	422 8	T08746	EST06638 Infant Brain,	6.31e-03	c 364	20	0.3	458 40	AQ164511	HS_3207_B2_F09_T7 CIT	1.19e-01
292	0.3	423 18	AA760097	vv69d12.r1 Stratagene	1.19e-01	c 365	20	0.3	460 38	B99867	CIT-HSP-2172D12.TR CIT	1.19e-01
293	0.3	424 40	AQ249250	T22p5-T7 TAMU Arabidop	1.19e-05	c 366	20	0.3	461 26	AI415844	fb34g10.x1 Zebrafish W	1.19e-01
294	0.3	424 21	AA979794	MEST0-D5.TW1412.Seq IS	1.19e-01	c 367	20	0.3	461 38	AQ019991	CIT-HSP-2312N21.TR CIT	1.19e-01
295	0.3	425 14	AA542570	fa08a06.s1 Zebrafish I	1.19e-01	c 368	20	0.3	461 21	AA948055	oe6f012.s1 NCI_CGAP_Lu	6.31e-03
296	0.3	425 23	AI113255	UI-R-Cp-nt-d-08-0-UI.	6.31e-03	c 369	21	0.3	462 41	AQ314921	CIT-HSP-202805.TP CIT	1.19e-01
297	0.3	426 33	N95743	Yy60g04.r1 Soares_mult	1.19e-01	c 370	22	0.3	463 41	AQ323085	RPC111-95J7.TJ RPC111	1.19e-01
298	0.3	426 34	W61462	md93g05.r1 Soares mous	6.31e-03	c 371	22	0.3	463 15	AA567483	HL01331.5Prime HL Dros	2.90e-04
299	0.3	426 22	AI046734	uh54e02.r1 Soares mous	1.19e-01	c 372	20	0.3	463 32	H98748	Yx12f10.s1 Soares mela	1.19e-01
300	0.3	427 10	AA222381	my17h03.r1 Barstead mo	1.19e-01	c 373	20	0.3	464 37	B40033	HS-1050-B2-E03-MR.abi	1.19e-01
301	0.3	430 39	AQ221444	HS_2004_B2_E05_P7 CIT	1.19e-01	c 374	20	0.3	464 38	AQ044233	CIT-HSP-233703.TR CIT	1.19e-01
302	0.3	430 37	B71933	RPC111-13K1.IV RPC111	1.19e-01	c 375	20	0.3				

522	21	0.3	528	9	AA176000	ms9905.r1 Soares mous	6.31e-03	595	20	0.3	597	18	AA803101	GM06994.5prime GM Dros	1.19e-01
523	21	0.3	529	41	AQ283869	RPC111-78C19.TJ RPC111	6.31e-03	596	20	0.3	597	37	FR0012562	F.rubripes GSS sequenc	1.19e-01
524	21	0.3	530	26	AA818627	UI-R-A0-aw-b-03-0-UI.s	6.31e-03	597	20	0.3	599	37	FR0012566	F.rubripes GSS sequenc	1.19e-01
525	21	0.3	530	20	AA956171	vx62a07.r1 Stratagene	6.31e-03	598	20	0.3	602	37	FR0031775	Fugu rubripes GSS sequ	1.19e-01
526	20	0.3	530	28	AA1562985	TENS2145 T. cruzi epim	1.19e-01	599	21	0.3	603	34	FR0026338	F.rubripes GSS sequenc	6.31e-03
527	20	0.3	533	38	B56766	CIT-HSP-2007M5.TPB CIT	1.19e-01	600	20	0.3	603	34	W72372	z62f07.s1 Soares.feta	1.19e-01
528	20	0.3	534	23	AI110047	GH0488.5prime GH Dros	1.19e-01	601	20	0.3	603	24	AI258156	LP01280.5prime LP Dros	1.19e-01
529	21	0.3	534	42	AQ405256	HS_5038.AL.B02.T7 RPCI	6.31e-03	602	21	0.3	605	37	FR02806	RPC111-10F18.TP RPC111	6.31e-03
530	20	0.3	534	40	AQ265429	CITBI-EL-2509020.TF CI	1.19e-01	603	20	0.3	605	37	FR0023876	F.rubripes GSS sequenc	1.19e-01
531	20	0.3	536	37	FR0031160	Fugu rubripes GSS sequ	1.19e-01	604	20	0.3	606	37	AG008998	Homo sapiens genomic D	6.31e-03
532	20	0.3	538	28	AI541873	SD07826.5prime SD Dros	1.19e-01	605	21	0.3	606	37	AG008998	Homo sapiens genomic D	6.31e-03
533	22	0.3	538	15	AA615307	vo01h05.r1 Stratagene	2.90e-04	606	20	0.3	608	41	AQ338864	RPC111-106J6.TJ RPC111	1.19e-01
534	21	0.3	541	27	AI426983	mm13b11.x1 Beddington	6.31e-03	607	21	0.3	608	28	AI543170	SD09809.5prime SD Dros	6.31e-03
535	20	0.3	542	41	AQ320052	RPC111-101F23.TV RPC11	1.19e-01	608	20	0.3	609	41	AQ328359	nxb0042N12f CUGI Rice	1.17e-05
536	20	0.3	542	41	AQ324259	RPC111-112C19.TV RPC11	1.19e-01	609	20	0.3	612	37	FR0032792	Fugu rubripes GSS sequ	1.19e-01
537	20	0.3	544	38	B93396	CIT-HSP-217B4.TR CIT-	1.19e-01	610	21	0.3	612	38	AQ061226	CIT-HSP-2352H9.TR CIT-	6.31e-03
538	21	0.3	547	40	AQ248087	HS_2015.AL.G06.MR CIT	6.31e-03	611	20	0.3	612	38	B56278	CITBI-EL-2530G16.TR CI	1.19e-01
539	20	0.3	548	20	AA9898110	NCM3B9T7 Mycelial Neur	1.19e-01	612	20	0.3	614	41	AQ354096	RPC111-ID2.TVB RPC111	1.19e-01
540	21	0.3	548	17	AA438832	LD13191.5prime LD Dros	1.19e-01	613	20	0.3	614	37	B63214	RPC111-ID2.TVB RPC111	1.19e-01
541	20	0.3	549	18	AA801162	EST190659 Normalized r	6.31e-03	614	20	0.3	614	37	FR0033208	Fugu rubripes GSS sequ	1.19e-01
542	21	0.3	550	42	AQ401887	HS_5046.B1.H03.T7 RPCI	6.31e-03	615	21	0.3	615	37	FR0018167	F.rubripes GSS sequenc	6.31e-03
543	20	0.3	550	20	AA908081	TENS0921 T. cruzi epim	1.19e-01	616	22	0.3	616	37	B18209	PHAC 2.34 re Mouse BAC	2.90e-04
544	20	0.3	551	28	AI510924	T7040.WVAT4 bloodstrea	1.19e-01	617	20	0.3	617	37	FR0003330	F.rubripes GSS sequenc	1.19e-01
545	24	0.3	552	41	AQ306865	HS_2196.B1.G09.MR CIT	4.19e-07	618	21	0.3	617	37	FR0034384	Fugu rubripes GSS sequ	6.31e-03
546	21	0.3	552	16	C76454	C76454 Mouse 3.5-dpc b	6.31e-03	619	21	0.3	617	37	FR0005249	F.rubripes GSS sequenc	6.31e-03
547	20	0.3	554	37	FR0029298	Fugu rubripes GSS sequ	1.19e-01	620	20	0.3	618	15	AA567321	HL01039.5prime HL Dros	1.19e-01
548	20	0.3	554	37	FR0002774	F.rubripes GSS sequenc	1.19e-01	621	20	0.3	618	37	FR0002429	F.rubripes GSS sequenc	1.19e-01
549	20	0.3	555	28	AI534169	SD06990.3prime SD Dros	1.19e-01	622	21	0.3	618	37	FR0020821	F.rubripes GSS sequenc	1.19e-01
550	21	0.3	558	25	AU038192	AU038192 Dictyostelium	6.31e-03	623	21	0.3	618	37	FR0003196	Fugu rubripes GSS sequ	6.31e-03
551	20	0.3	559	26	AI413460	me77c01.x1 Soares mous	1.19e-01	624	20	0.3	618	37	FR0033612	Fugu rubripes GSS sequ	1.19e-01
552	20	0.3	560	38	B53265	CIT-HSP-2009K7.TF CIT-	1.19e-01	625	20	0.3	618	37	FR0007983	F.rubripes GSS sequenc	1.19e-01
553	20	0.3	561	21	AA942935	EST198434 Normalized r	1.19e-01	626	20	0.3	618	37	FR0013834	F.rubripes GSS sequenc	1.19e-01
554	22	0.3	563	37	B03625	CSRL-183G4-u CSRL flow	2.90e-04	627	20	0.3	619	37	FR0002393	F.rubripes GSS sequenc	1.19e-01
555	20	0.3	564	37	FR0022187	F.rubripes GSS sequenc	1.19e-01	628	20	0.3	619	37	FR0003792	F.rubripes GSS sequenc	1.19e-01
556	20	0.3	567	42	AQ379945	RPC111-163H11.TJ RPC11	1.19e-01	629	22	0.3	619	37	FR0032711	Fugu rubripes GSS sequ	2.90e-04
557	20	0.3	568	37	FR0010102	F.rubripes GSS sequenc	1.19e-01	630	20	0.3	619	37	FR0008519	F.rubripes GSS sequenc	1.19e-01
558	20	0.3	568	39	AQ014272	RPC111-22H3.TKBF RPC11	1.19e-01	631	20	0.3	619	37	FR0003801	F.rubripes GSS sequenc	1.19e-01
559	20	0.3	569	25	AU040159	AU040159 Mouse four-ce	1.19e-01	632	20	0.3	619	37	FR0006470	F.rubripes GSS sequenc	1.19e-01
560	20	0.3	569	9	AA222121	my29g10.r1 Barstead mo	1.19e-01	633	20	0.3	623	39	AQ108802	CIT-HSP-2372G1.TR CIT	1.19e-01
561	20	0.3	569	42	AQ227566	RPC111-141B18.TJ RPC11	1.19e-01	634	20	0.3	623	39	AA759928	vv32g11.r1 Stratagene	1.19e-01
562	20	0.3	570	37	FR0009543	F.rubripes GSS sequenc	1.19e-01	635	20	0.3	624	37	AG011641	Homo sapiens genomic D	1.19e-01
563	21	0.3	571	40	AQ239499	CIT-HSP-2386N1.TF.1 CI	6.31e-03	636	21	0.3	625	37	AG008999	Homo sapiens genomic D	6.31e-03
564	20	0.3	572	42	AQ421867	RPC11-11-168C9.TJ RPCI-	1.19e-01	637	23	0.3	625	38	B64278	CIT-HSP-2022E3.TF CIT-	1.17e-05
565	20	0.3	572	36	AA082619	no41b08.r1 Stratagene	1.19e-01	638	20	0.3	625	37	AG008999	Homo sapiens genomic D	1.19e-01
566	20	0.3	574	15	AA604994	no73f02.s1 NCI.CGAP_AA	1.19e-01	639	20	0.3	626	14	AA539914	LD19214.5prime LD Dros	1.19e-01
567	20	0.3	576	22	AI052139	oy30d08.x1 Soarespara	1.19e-01	640	20	0.3	626	37	AG012222	Homo sapiens genomic D	1.19e-01
568	20	0.3	576	20	AA919115	AI85g11.s1 NCI.CGAP.Ki	1.19e-01	641	21	0.3	629	37	AG009011	Homo sapiens genomic D	6.31e-03
569	21	0.3	576	42	AQ417346	RPC11-11-188E9.TV RPCI-	6.31e-03	642	22	0.3	630	34	W67899	z42a06.r1 Soares.feta	2.90e-04
570	20	0.3	576	18	AA760852	n214f11.s1 NCI.CGAP_GC	1.19e-01	643	21	0.3	632	38	AQ020815	CIT-HSP-2310H13.TR CIT	6.31e-03
571	20	0.3	577	39	AQ083665	CPG05664A CPlOWAGNAL C	1.19e-01	644	20	0.3	632	24	AU033646	AU033646 Dictyostelium	1.19e-01
572	20	0.3	578	42	AQ441833	HS_5106.B1.E01.T7A RPC	1.19e-01	645	20	0.3	632	28	AI534159	SD06578.5prime SD Dros	1.19e-01
573	20	0.3	579	16	C78218	C78218 Mouse 3.5-dpc b	1.19e-01	646	20	0.3	632	40	AQ243426	HS_2058.A2.G01.MR CIT	1.19e-01
574	20	0.3	579	24	AI260592	LP04519.5prime LP Dros	1.19e-01	647	20	0.3	633	17	AA735368	LD21193.5prime LD Dros	1.19e-01
575	20	0.3	581	37	FR0002742	F.rubripes GSS sequenc	1.19e-01	648	21	0.3	634	20	C91198	C91198 Dictyostelium d	6.31e-03
576	20	0.3	583	37	B06412	CSRL-80a9-u CSRL flow	1.19e-01	649	20	0.3	634	25	AI237857	LP12884.3prime LP Dros	1.19e-01
577	20	0.3	583	37	FR0021168	F.rubripes GSS sequenc	1.19e-01	650	20	0.3	635	39	AG008908	RPC111-22K17.TVB RPCI	1.19e-01
578	21	0.3	583	20	C90163	C90163 Dictyostelium d	6.31e-03	651	20	0.3	635	37	AG008997	Homo sapiens genomic D	1.19e-01
579	20	0.3	584	24	AI222373	gg98a05.x1 Soares.NFL	1.19e-01	652	21	0.3	637	38	AQ075108	CIT-HSP-2353L5.TR CIT-	6.31e-03
580	20	0.3	584	41	AQ335355	HS_5016.B2.G12.SP6E RP	1.19e-01	653	20	0.3	638	41	AQ320770	RPC111-92E22.TV RPC111	1.19e-01
581	20	0.3	585	30	AA920306	vx93g09.r1 Soares 2NM	1.19e-01	654	20	0.3	647	37	AG012221	Homo sapiens genomic D	1.19e-01
582	20	0.3	585	39	AQ202050	RPC111-45J14.TK RPC111	1.19e-01	655	20	0.3	647	41	AQ355933	CITBI-EL-2532A18.TF CI	1.19e-01
583	20	0.3	585	22	AU016721	AU016721 Mouse two-ceb	1.19e-01	656	20	0.3	649	37	B71494	RPC111-8N9.TP RPC111 H	1.19e-01
584	21	0.3	586	37	FR0021323	F.rubripes GSS sequenc	6.31e-03	657	20	0.3	650	26	AU002712	AU002712 Bombyx mori p	1.19e-01
585	20	0.3	587	37	FR0024133	F.rubripes GSS sequenc	1.19e-01	658	20	0.3	650	37	AG014567	Homo sapiens genomic D	1.19e-01
586	21	0.3	587	41	AQ332027	HS_5002.B1.C09.T7 RPCI	6.31e-03	659	21	0.3	650	36	AA118174	mm13b11.r1 Beddington	6.31e-03
587	21	0.3	588	25	AI327289	mp56b11.x1 Soares 2NM	6.31e-03	660	20	0.3	652	41	AQ283476	RPC111-79C11.TV RPC111	1.19e-01
588	20	0.3	588	42	AQ414581	RPC11-11-177C3.TJ RPCI-	1.19e-01	661	20	0.3	652	28	AI544955	LD46602.5prime LD Dros	1.19e-01
589	20	0.3	589	37	FR0011084	F.rubripes GSS sequenc	1.19e-01	662	21	0.3	654	37	AG015611	Homo sapiens genomic D	6.31e-03
590	20	0.3	591	24	AQ033763	AU033763 Dictyostelium	1.19e-01	663	20	0.3	658	9	AA186034	mt35h02.r1 Soares mous	1.19e-01
591	20	0.3	592	37	B62733	T20K16TF.1 TAMU Arabid	1.19e-01	664	20	0.3	659	37	AG012244	Homo sapiens genomic D	1.19e-01
592	20	0.3	592	39	AQ201178	RPC111-46M8.TJ RPC111	1.19e-01	665	20	0.3	660	41	AQ347480	RPC111-126I4.TJ RPC111	1.19e-01
593	20	0.3	593	32	N23817	YX36f12.r1 Soares.mela	1.19e-01	666	21	0.3	661	41	AQ286662	RPC111-76B9.TJ RPC111	6.31e-03
594	20	0.3	594	38	AQ044107	CIT-HSP-2318P22.TF CIT	1.19e-01	667	20	0.3	663	24	AA8031688	GM13983.5prime GM Dros	1.19e-01

C 668	23	0.3	664 41	AQ289098	nbxb0034M17f CUGI Rice	1.17e-05	19	0.2	271 40	AQ278873	CITBT-EI-2523D18.TR CI	1.91e+00
C 669	20	0.3	669 39	AQ014227	RPC111-22K17.TKBCF RPC	1.19e-01	19	0.2	278 41	AQ344015	RPC111-124J9.TV RPC111	1.91e+00
C 670	21	0.3	676 34	AAU00678	mg33f01.r1 Soares mous	6.31e-03	19	0.2	279 9	AA168740	ms34a02.r1 Stratagene	1.91e+00
C 671	20	0.3	676 26	AAU002893	AU002893 Bombyx mori p	1.19e-01	19	0.2	279 40	AA268218	RPC111-73L8.TJ RPC111	1.91e+00
C 672	22	0.3	677 42	AQ25634	CITBT-EI-2556B7.TF CIT	2.90e-04	19	0.2	288 28	AA1508764	vc21f11.y1 Ko mouse em	1.91e+00
C 673	23	0.3	677 17	AA697360	HL02318.Sprime HL Dros	1.17e-05	19	0.2	289 15	AA606720	vc07c04.r1 Stratagene	1.91e+00
C 674	20	0.3	679 42	AQ415324	RPC11-11-165D17.TJ RPCI	1.19e-01	19	0.2	292 28	AA1508769	vc22b03.y1 Ko mouse em	1.91e+00
C 675	20	0.3	679 33	WQ2556	za49h01.r1 Soares feta	1.19e-01	19	0.2	292 25	AA680741	LnFrAm0250 Leishmania	1.91e+00
C 676	20	0.3	685 42	AQ417081	RPC1-11-177K16.TV RPCI	1.19e-01	19	0.2	293 36	AA678367	7P02D11 Chromosome 7 P	1.91e+00
C 677	20	0.3	687 37	AG007660	Homo sapiens genomic D	1.19e-01	19	0.2	295 16	AA675476	vr72d01.s1 Knowles Sol	1.91e+00
C 678	20	0.3	689 24	AQ034828	AU034828 Dictyostelium	1.19e-01	19	0.2	299 9	AA167157	zp06f03.r1 Stratagene	1.91e+00
C 679	21	0.3	689 17	AA754976	vu59g05.r1 Soares mous	6.31e-03	19	0.2	304 11	AA907379	OK95e02.s1 NCI.CGAP Lu	1.91e+00
C 680	20	0.3	691 37	AG007659	Homo sapiens genomic D	1.19e-01	19	0.2	308 20	AA334945	EST39226 Embryo, 9 wee	1.91e+00
C 681	20	0.3	696 37	AG007658	Homo sapiens genomic D	1.19e-01	19	0.2	309 31	H27701	Y161c12.r1 Soares brea	1.91e+00
C 682	20	0.3	698 40	AQ263380	CITBT-EI-2503H5.TF CIT	1.19e-01	19	0.2	309 37	FR0004818	F.rubripes GSS sequenc	1.91e+00
C 683	20	0.3	702 25	AQ039558	AU039558 Dictyostelium	1.19e-01	19	0.2	310 37	FR0029693	Fugu rubripes GSS sequ	1.91e+00
C 684	20	0.3	708 24	AQ034494	AU034494 Dictyostelium	1.19e-01	19	0.2	315 20	AA863841	vx09f06.r1 Soares 2Nm	1.91e+00
C 685	20	0.3	709 24	AQ033788	AU033788 Dictyostelium	1.19e-01	19	0.2	322 36	AA171747	mo62d04.r1 Stratagene	1.91e+00
C 686	21	0.3	710 18	AA798410	vy06e08.r1 Stratagene	6.31e-03	19	0.2	324 39	AQ084946	HS.2265.B2.C10.MF.CIT	1.91e+00
C 687	20	0.3	713 21	AA981409	U996C05.r1 Soares mous	1.19e-01	19	0.2	326 27	AA157887	tj48a01.x1 Soares NSF	1.91e+00
C 688	21	0.3	718 38	AQ079291	CIT-HSP-2365K18.TR CIT	6.31e-03	19	0.2	328 26	AA1387168	GH17619.Sprime GH Dros	1.91e+00
C 689	20	0.3	719 41	AQ362378	nbxb0049p21r CUGI Rice	1.19e-01	19	0.2	329 25	AA046128	AU046128 Mouse sixteen	1.91e+00
C 690	20	0.3	721 24	AQ033551	AU033551 Dictyostelium	1.19e-01	19	0.2	329 13	AA040995	EST01811 Mouse 7.5 dpc	1.91e+00
C 691	20	0.3	723 24	AQ033533	AU033533 Dictyostelium	1.19e-01	19	0.2	329 35	AA058418	zk81e01.r1 Soares Preg	1.91e+00
C 692	20	0.3	723 37	AG001964	Homo sapiens genomic D	1.19e-01	19	0.2	331 39	AQ086321	HS.2166.B1.F06.MF.CIT	1.91e+00
C 693	20	0.3	724 37	AG009112	Homo sapiens genomic D	1.19e-01	19	0.2	335 28	AA1506626	vn47e04.x1 Barstead mo	1.91e+00
C 694	20	0.3	729 37	AG009113	Homo sapiens genomic D	1.19e-01	19	0.2	335 15	AA582524	nn508606.s1 NCI.CGAP_KI	1.91e+00
C 695	21	0.3	740 20	C84093	C84093 Dictyostelium d	6.31e-03	19	0.2	345 38	AQ004401	CIT-HSP-2295L19.TR CIT	1.91e+00
C 696	20	0.3	740 40	AQ269380	HS_2007.AL.G03.T7 CIT	1.19e-01	19	0.2	345 25	AA1289936	qv02h10.x1 NCI.CGAP_KI	1.91e+00
C 697	20	0.3	752 21	AA951110	LD31410.Sprime LD Dros	1.19e-01	19	0.2	346 17	AA1717368	vp42g10.r1 Barstead mo	1.91e+00
C 698	20	0.3	754 40	AQ273724	nbxb0030D18r CUGI Rice	1.19e-01	19	0.2	348 24	AA1567063	tp49g02.x1 NCI.CGAP_Ut	1.91e+00
C 699	20	0.3	760 27	AA177982	fb49h08.x1 Zebrafish W	1.19e-01	19	0.2	348 28	AA680796	LnFrAm0333 Leishmania	1.91e+00
C 700	21	0.3	782 25	AA127282	mo62h06.x1 Stratagene	6.31e-03	19	0.2	351 36	AA137632	mq99d03.r1 Soares mous	1.91e+00
C 701	20	0.3	786 24	AQ033453	AU033453 Dictyostelium	1.19e-01	19	0.2	351 37	FR0009367	F.rubripes GSS sequenc	1.91e+00
C 702	20	0.3	813 24	AQ033632	AU033632 Dictyostelium	1.19e-01	19	0.2	351 40	AQ165716	HS.3065.B1.F09.MR CIT	1.91e+00
C 703	20	0.3	818 15	AA068727	ae56e09.s1 Stratagene	1.19e-01	19	0.2	352 29	AA1568849	t023a10.x1 NCI.CGAP_Ut	1.91e+00
C 704	20	0.3	820 42	AA050452	nbxb0004aF05r CUGI Ric	1.19e-01	19	0.2	353 9	AA166094	ms23e07.r1 Stratagene	1.91e+00
C 705	21	0.3	823 25	AA123807	mm74b12.x1 Stratagene	6.31e-03	19	0.2	355 41	AQ356090	CITBT-EI-2529B20.TR CI	1.91e+00
C 706	20	0.3	835 17	AA697762	HL03118.Sprime HL Dros	1.19e-01	19	0.2	356 16	AA673751	vs64e06.r1 Stratagene	1.91e+00
C 707	20	0.3	880 37	B13213	F22F23-Sp6 IGF Arabidop	1.19e-01	19	0.2	359 42	AQ385862	RPC111-142M22.TJ RPC11	1.91e+00
C 708	21	0.3	912 37	B13263	F26G16-T7 IGF Arabidop	6.31e-03	19	0.2	360 20	AA907053	cm10907.s1 Soares_NFL	1.91e+00
C 709	21	0.3	915 37	B13200	T19M22-T7 TAMU Arabidop	6.31e-03	19	0.2	361 9	AA221362	mw11h07.r1 Soares mous	1.91e+00
C 710	22	0.3	934 18	AA765056	ca7a411.s1 NCI.CGAP_GC	2.90e-04	19	0.2	362 22	AU023132	AU023132 Mouse unferti	1.91e+00
C 711	20	0.3	980 39	AF010974	Homo sapiens chromosom	1.19e-01	19	0.2	364 31	H65043	Yr69p11.r1 Soares feta	1.91e+00
C 712	20	0.3	1064 22	AA108630	mgae0003CDU5f Magnapor	1.19e-01	19	0.2	365 28	AA1551793	vo84h12.x1 Barstead mo	1.91e+00
C 713	21	0.3	1120 37	B11801	T4M23-Sp6 TAMU Arabidop	6.31e-03	19	0.2	366 33	N72930	YV47f09.r1 Soares feta	1.91e+00
C 714	20	0.3	1189 38	AQ034099	1(3)j8C8 Drosophila me	1.19e-01	19	0.2	366 31	H32652	EST107948 Rat PC-12 ce	1.91e+00
C 715	20	0.3	1234 20	AF012875	AF012875 Bovine fetal	1.19e-01	19	0.2	367 26	AA1453308	mc02f08.x1 Soares mous	1.91e+00
C 716	23	0.3	1577 23	AF083305	AF083305 Drosophila me	1.17e-05	19	0.2	369 39	AQ088386	HS.3000.A2.F01.MR CIT	1.91e+00
C 717	21	0.3	1801 42	AF101710	Homo sapiens chromosom	6.31e-03	19	0.2	369 12	AA365428	EST76462 Pineal gland	1.91e+00
C 718	21	0.3	6921 41	AF101618	Homo sapiens chromosom	6.31e-03	19	0.2	370 19	R00591	ye74b01.r1 Soares feta	1.91e+00
C 719	19	0.2	105 37	FR0022757	F.rubripes GSS sequenc	1.91e+00	19	0.2	371 8	D27614	CELK015D5R Yuj1 Kohara	1.91e+00
C 720	19	0.2	121 18	AA834402	cf67h01.s1 NCI.CGAP-Co	1.91e+00	19	0.2	371 22	AA0266711	os87f01.x1 Soares_sene	1.91e+00
C 721	19	0.2	130 17	AA717013	vu61c10.r1 Soares mous	1.91e+00	19	0.2	372 38	AQ025890	1(2)K09217 Drosophila	1.91e+00
C 722	19	0.2	146 38	B82384	RPC111-15C2.TPB RPC111	1.91e+00	19	0.2	372 27	AA1049734	LnLv39p10/413D Leishma	1.91e+00
C 723	19	0.2	148 40	AQ267084	RPC111-72L4.TJ RPC111	1.91e+00	19	0.2	377 26	AA159133	mr67a02.x1 Stratagene	1.91e+00
C 724	19	0.2	169 22	AA066368	TENU2484 T. cruzi epim	1.91e+00	19	0.2	378 38	AQ065235	q226a01.x1 NCI.CGAP_Br	1.91e+00
C 725	19	0.2	176 9	AA180556	MBACFCF7F02r3 Brugia ma	1.91e+00	19	0.2	379 18	AA773548	ab57h10.s1 Stratagene	1.91e+00
C 726	19	0.2	180 33	N73077	za08c02.s1 Soares mela	1.91e+00	19	0.2	380 27	AA1467078	vd09g10.x1 Knowles Sol	1.91e+00
C 727	19	0.2	207 8	T40481	Yr02a01.s1 Stratagene	1.91e+00	19	0.2	381 39	AQ122959	HS.3094.B1.H01.MR CIT	1.91e+00
C 728	19	0.2	216 10	AA250810	zs06a03.s1 NCI.CGAP_GC	1.91e+00	19	0.2	381 40	AQ166244	HS.3076.B1.D02.MR CIT	1.91e+00
C 729	19	0.2	222 38	AQ033150	CIT-HSP-2204A20.TR CIT	1.91e+00	19	0.2	382 16	AA617185	vj79a01.r1 Knowles Sol	1.91e+00
C 730	19	0.2	231 23	AA175697	EST12928 Normalized r	1.91e+00	19	0.2	383 26	AA137484	qu01g06.x1 NCI.CGAP-Co	1.91e+00
C 731	19	0.2	234 19	T86625	Y081a03.r1 Soares feta	1.91e+00	19	0.2	383 15	AA571266	v190e10.r1 Stratagene	1.91e+00
C 732	19	0.2	237 38	AQ066938	HS_2228.AL.B10.MF CIT	1.91e+00	19	0.2	386 17	AA730643	nw42h12.s1 NCI.CGAP_Ew	1.91e+00
C 733	19	0.2	239 19	T66910	Yr50f11.s1 Soares feta	1.91e+00	19	0.2	387 39	AQ118356	HS.3004.A1.F11.MR CIT	1.91e+00
C 734	19	0.2	242 42	AQ351105	RPC111-152D6.TJ RPC111	1.91e+00	19	0.2	388 20	AA890534	ak11b11.s1 Soares para	1.91e+00
C 735	19	0.2	248 28	AA1536307	na84h09.y1 Soares mous	1.91e+00	19	0.2	389 15	AA575448	v190b01.r1 Stratagene	1.91e+00
C 736	19	0.2	250 14	AA498860	v182h07.r1 Stratagene	1.91e+00	19	0.2	390 19	R23476	YH39e04.r1 Soares Plac	1.91e+00
C 737	19	0.2	251 8	AA747581	nx92d12.s1 NCI.CGAP_GC	1.91e+00	19	0.2	392 41	AQ301018	HS_3105.A2.H01.MR CIT	1.91e+00
C 738	19	0.2	261 7	T17109	NIB340 Normalized inf	1.91e+00	19	0.2	394 13	AA414554	vc60f11.s1 Knowles Sol	1.91e+00
C 739	19	0.2	262 38	B93088	CIT-HSP-2173J15.TF CIT	1.91e+00	19	0.2	395 27	AA957628	UI-R-EI-gf-a-01-0-UI.s	1.91e+00
C 740	19	0.2	270 14	AA525815	n161c05.s1 NCI.CGAP_Ov	1.91e+00	19	0.2				

814	19	0.2	401 27	AI423354	ms88a04.x1 Stratagene	1.91e+00	887	19	0.2	480 32	H71452	yu71b05.s1 Weizmann Ol	1.91e+00
815	19	0.2	401 42	AQ45401	GSTC01195 Trypanosoma	1.91e+00	888	19	0.2	481 21	AA993885	ou02h09.s1 Soares_tota	1.91e+00
816	19	0.2	404 38	AQ39804	CIT-HSP-232324.TF CIT	1.91e+00	889	19	0.2	487 21	AI015955	ou30a10.x1 Soares_test	1.91e+00
817	19	0.2	406 16	AA646074	vn09c04.r1 Stratagene	1.91e+00	890	19	0.2	489 42	AQ444673	GSTC01932 Trypanosoma	1.91e+00
818	19	0.2	408 9	AA158769	zo63h06.s1 Stratagene	1.91e+00	891	19	0.2	490 41	AQ354677	CITBI-E1-2538A4.TF CIT	1.91e+00
819	19	0.2	408 17	AA726533	vu92h10.r1 Stratagene	1.91e+00	892	19	0.2	493 17	AA714930	nv49c05.r1 NCI-CGAP_Ew	1.91e+00
820	19	0.2	408 19	T98528	ye70809.r1 Soares	1.91e+00	893	19	0.2	494 27	AA957703	UI-R-E1-fw-g-10-0-UI.s	1.91e+00
821	19	0.2	413 25	AA043874	AU043874 Mouse sixteen	1.91e+00	894	19	0.2	495 26	AA956887	UI-R-E1-fr-a-06-0-UI.s	1.91e+00
822	19	0.2	413 17	AA063962	z153e02.s1 Soares_feta	1.91e+00	895	19	0.2	495 38	BS0693	CIT-HSP-581010.TP CIT	1.91e+00
823	19	0.2	414 8	T17124	NIB357 Normalized inf	1.91e+00	896	19	0.2	501 25	AI330436	fa92f10.x1 zebrafish f	1.91e+00
824	19	0.2	414 39	AQ131155	HS_3036.A1.G05.MR CIT	1.91e+00	897	19	0.2	501 40	AQ267939	RPC111-72K14.TK RPC111	1.91e+00
825	19	0.2	414 37	B44934	HS_1060-A2-C12-MF abi	1.91e+00	898	19	0.2	501 28	AI546767	BSML3S212G20SK Brugia	1.91e+00
826	19	0.2	414 28	AI545075	ff70406.y1 Zebrafish W	1.91e+00	899	19	0.2	504 31	H29383	vm32h03.r1 Soares inf	1.91e+00
827	19	0.2	415 30	H03010	YJ50f03.r1 Soares plac	1.91e+00	900	19	0.2	505 40	AQ190318	HS_3223.A1.G11.T7 CIT	1.91e+00
828	19	0.2	420 42	AQ43292	HS_5050.A2.H10.SP6E RP	1.91e+00	901	19	0.2	505 40	AQ182989	HS_3123.B1.B02.T7 CIT	1.91e+00
829	19	0.2	420 13	AA453131	zx38f04.r1 Soares_tota	1.91e+00	902	19	0.2	506 20	AA862021	AI46d04.s1 NCI-CGAP_Ew	1.91e+00
830	19	0.2	421 26	AI384699	fb08b08.r1 zebrafish f	1.91e+00	903	19	0.2	507 28	AI505229	vg76a03.x1 Knowles Sol	1.91e+00
831	19	0.2	422 21	AI008726	EST203177 Normalized r	1.91e+00	904	19	0.2	509 41	AQ341248	RPC111-120B24.TJ RPC11	1.91e+00
832	19	0.2	424 41	AQ336272	HS_5019.B1.D10.SP6E RP	1.91e+00	905	19	0.2	512 8	T03771	IB877 Infant brain, Be	1.91e+00
833	19	0.2	425 20	AA892792	EST196595 Normalized r	1.91e+00	906	19	0.2	513 42	AQ426297	CITBI-E1-2563C20.TR CI	1.91e+00
834	19	0.2	427 39	AQ109795	CIT-HSP-2378K9.TF CIT	1.91e+00	907	19	0.2	514 16	AA677682	zj7f10.s1 Soares_feta	1.91e+00
835	19	0.2	428 39	AQ222983	HS_2017.A2.D03.T7 CIT	1.91e+00	908	19	0.2	516 18	AA778401	zf95g12.s1 Soares_feta	1.91e+00
836	19	0.2	428 18	AA797134	vn43f03.r1 Stratagene	1.91e+00	909	19	0.2	516 41	AQ347929	RPC111-10516.TV RPC111	1.91e+00
837	19	0.2	429 36	AA085388	zn07c05.s1 Stratagene	1.91e+00	910	19	0.2	517 37	FR0022225	F.rubripes GSS sequenc	1.91e+00
838	19	0.2	429 28	AI588652	fb68h05.y1 Zebrafish W	1.91e+00	911	19	0.2	521 42	AQ446555	GSTC01913 Trypanosoma	1.91e+00
839	19	0.2	431 27	AI428447	mo20b01.x1 Life Tech m	1.91e+00	912	19	0.2	523 14	AA528455	ne84f05.s1 NCI-CGAP_Ew	1.91e+00
840	19	0.2	432 18	AA768786	oc17g05.s1 NCI-CGAP_GC	1.91e+00	913	19	0.2	524 41	AQ358692	HS_5029.A2.B06.T7 RPI	1.91e+00
841	19	0.2	433 42	AQ431120	HS_5130.A1.A03.SP6E RP	1.91e+00	914	19	0.2	527 41	AQ356331	CITBI-E1-2536B12.TF CI	1.91e+00
842	19	0.2	434 42	AQ433371	HS_2231.B2.H12.MF CIT	1.91e+00	915	19	0.2	527 40	AQ189618	HS_3219.B1.G06.T7 CIT	1.91e+00
843	19	0.2	434 41	AQ333759	HS_5019.A2.B09.SP6E RP	1.91e+00	916	19	0.2	528 41	AQ322497	RPC111-99C12.TJ RPC111	1.91e+00
844	19	0.2	434 27	AI450873	ms01h09.x1 Stratagene	1.91e+00	917	19	0.2	528 20	AA892868	EST196671 Normalized r	1.91e+00
845	19	0.2	435 32	N34514	YJ55b03.s1 Soares_mult	1.91e+00	918	19	0.2	530 39	AQ118624	HS_3019.B1.C11.T7 CIT	1.91e+00
846	19	0.2	436 27	AI471654	TJ99a06.x1 NCI-CGAP_Co	1.91e+00	919	19	0.2	530 21	AA943550	EST199049 Normalized r	1.91e+00
847	19	0.2	437 36	AA139861	mq95b01.r1 Stratagene	1.91e+00	920	19	0.2	531 41	AQ322899	RPC111-11K16.TJ RPC11	1.91e+00
848	19	0.2	438 37	FR0015956	F.rubripes GSS sequenc	1.91e+00	921	19	0.2	531 39	AQ206538	HS_3234.A2.F01.T7 CIT	1.91e+00
849	19	0.2	438 38	AQ041227	CIT-HSP-2338H17.TF CIT	1.91e+00	922	19	0.2	533 41	AQ314055	RPC111-104P5.TJ RPC111	1.91e+00
850	19	0.2	439 28	AI060605	vi24f02.x1 Stratagene	1.91e+00	923	19	0.2	542 35	C06380	C06380 Human pancreat	1.91e+00
851	19	0.2	440 8	T48875	Y05h08.r1 Stratagene	1.91e+00	924	19	0.2	544 38	AQ008537	CIT-HSP-2283F22.TRB CI	1.91e+00
852	19	0.2	442 21	AI021889	ow96a05.x1 Soares_feta	1.91e+00	925	19	0.2	548 37	B72527	RPC111-9E12.TV RPC111	1.91e+00
853	19	0.2	444 33	N62273	Y898d12.s1 Soares_mult	1.91e+00	926	19	0.2	550 38	B94288	CIT-HSP-2166L11.TF CIT	1.91e+00
854	19	0.2	446 15	AA605872	fa20g08.r1 Bpkrearily	1.91e+00	927	19	0.2	557 41	AQ357255	CITBI-E1-2534P6.TR CIT	1.91e+00
855	19	0.2	447 31	H41204	Yn88f12.r1 Soares adul	1.91e+00	928	19	0.2	560 37	FR0033997	Fugu rubripes GSS sequ	1.91e+00
856	19	0.2	448 24	W37349	zc09b12.s1 Soares_para	1.91e+00	929	19	0.2	562 22	A1034990	TENG0050 T. cruzi epim	1.91e+00
857	19	0.2	449 32	AI042756	uc75c04.x1 Sugano mous	1.91e+00	930	19	0.2	562 39	AQ003316	RPC111-20D6.TPB RPC111	1.91e+00
858	19	0.2	450 35	AA050579	mlj16e10.r1 Soares mous	1.91e+00	931	19	0.2	566 42	AQ425164	CITBI-E1-2561F9.TF CIT	1.91e+00
859	19	0.2	450 19	T97794	ye54b05.r1 Soares feta	1.91e+00	932	19	0.2	568 9	AA152939	mr16b07.r1 Soares mous	1.91e+00
860	19	0.2	451 32	N30929	Yx50d03.r1 Soares feta	1.91e+00	933	19	0.2	571 26	AI388902	GHI9936.5prime GH Dros	1.91e+00
861	19	0.2	452 42	AQ390027	RPC111-158O23.TV RPC11	1.91e+00	934	19	0.2	571 41	AQ334270	HS_5005.A2.E11.T7 RPI	1.91e+00
862	19	0.2	452 10	AA269904	va60e12.r1 Soares mous	1.91e+00	935	19	0.2	572 36	AA120692	mp72g10.r1 Soares 2Nbm	1.91e+00
863	19	0.2	455 38	AQ015629	CIT-HSP-2309N17.TR CIT	1.91e+00	936	19	0.2	581 8	T48132	Yb25b11.s1 Stratagene	1.91e+00
864	19	0.2	457 17	AA739114	vv66f05.r1 Stratagene	1.91e+00	937	19	0.2	585 37	B72188	RPC111-7K22.TP RPC111	1.91e+00
865	19	0.2	459 15	AA596343	vo30b11.r1 Barstead mo	1.91e+00	938	19	0.2	588 16	C81242	C81242 Mouse 3.5-dpc b	1.91e+00
866	19	0.2	459 9	AA172697	ms19b08.r1 Stratagene	1.91e+00	939	19	0.2	589 37	FR0008663	F.rubripes GSS sequenc	1.91e+00
867	19	0.2	459 16	AA646320	vn12a02.r1 Stratagene	1.91e+00	940	19	0.2	590 18	C87122	C87122 Mouse fertilize	1.91e+00
868	19	0.2	460 13	AA475029	vh03g01.r1 Soares mous	1.91e+00	941	19	0.2	593 40	AQ266909	RPC111-74N5.TJ RPC111	1.91e+00
869	19	0.2	461 21	AI010917	EST203368 Normalized r	1.91e+00	942	19	0.2	594 37	FR0033784	Fugu rubripes GSS sequ	1.91e+00
870	19	0.2	464 22	AI035156	TENG0247 T. cruzi epim	1.91e+00	943	19	0.2	596 26	AI387954	GHI8664.5prime GH Dros	1.91e+00
871	19	0.2	465 12	AA387138	vc22b03.r1 Ko mouse em	1.91e+00	944	19	0.2	597 38	AQ039681	CIT-HSP-2327G17.TF CIT	1.91e+00
872	19	0.2	467 37	B16425	34ZD12.TVB CIT978SKAL	1.91e+00	945	19	0.2	597 38	AQ061567	CIT-HSP-2348K13.TF CIT	1.91e+00
873	19	0.2	468 21	AI018216	ou16c01.x1 Soares_NFL	1.91e+00	946	19	0.2	597 37	FR0011107	F.rubripes GSS sequenc	1.91e+00
874	19	0.2	468 37	B36396	HS-1040-B2-A03-MF abi	1.91e+00	947	19	0.2	601 9	AA210244	mo84h07.r1 Beddington	1.91e+00
875	19	0.2	468 37	B34315	HS-1024-B1-B05-WR.abi	1.91e+00	948	19	0.2	601 42	AQ380584	RPC111-166Q24.TJ RPC11	1.91e+00
876	19	0.2	468 15	AA591808	vi49b11.r1 Beddington	1.91e+00	949	19	0.2	602 38	BS9606	CIT-HSP-342K15.TPB CIT	1.91e+00
877	19	0.2	470 39	AQ222719	HS_2012.A2.H07.T7 CIT	1.91e+00	950	19	0.2	604 35	AA304011	z106c10.r1 Soares_feta	1.91e+00
878	19	0.2	470 9	AA172873	ms20d02.r1 Stratagene	1.91e+00	951	19	0.2	605 40	AQ266522	RPC111-75A2.TJ RPC111	1.91e+00
879	19	0.2	475 25	AI334310	qq25g12.x1 Soares_NHMH	1.91e+00	952	19	0.2	607 42	AQ394562	CITBI-E1-2553M14.TF CI	1.91e+00
880	19	0.2	475 21	AI004186	ou56d10.x1 NCI-CGAP_Br	1.91e+00	953	19	0.2	610 35	AA034012	z106c10.s1 Soares_feta	1.91e+00
881	19	0.2	478 24	AZ205185	ap13c07.x1 Schiller ol	1.91e+00	954	19	0.2	617 39	AQ208264	HS_3219.A1.C06.T7 CIT	1.91e+00
882	19	0.2	478 32	N24387	Yx14f02.r1 Soares mela	1.91e+00	955	19	0.2	618 40	AQ265832	CITBI-E1-2503L11.TR CI	1.91e+00
883	19	0.2	478 33	N67876	Yz52b01.s1 Horton Feta	1.91e+00	956	19	0.2	618 37	FR0002343	F.rubripes GSS sequenc	1.91e+00
884	19	0.2	479 40	AQ186282	HS_3083.B2.H03.MF CIT	1.91e+00	957	19	0.2	618 37	FR0004638	F.rubripes GSS sequenc	1.91e+00
885	19	0.2	479 37	AF017579	Homo sapiens YAC 307A1	1.91e+00	958	19	0.2	619 37	FR0005223	F.rubripes GSS sequenc	1.91e+00
886	19	0.2	479 36	AA109538	mm01h03.r1 Stratagene	1.91e+00	959	19	0.2	619 37	FR0032807	Fugu rubripes GSS sequ	1.91e+00


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Query Match
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 TAAATCGAAATCAAAATCGTACTCTGACTACGGGTCTAGTAGAGAGGTCAACCATCAGCCG 61
|||||
Qy 2169 TAAATCGAAATCAAAATCGTACTCTGACTACGGGTCTAGTAGAGAGGTCAACCATCAGCCG 2228
|||||

Db 62 AAGATGATGCGTCAAGATAGAGAGAGTCTCTAGAGAGGACATTATGATGTTCTCTAGT 121
|||||
Qy 2229 AAGATGATGCGTCAAGATAGAGAGAGTCTCTAGAGAGGACATTATGATGTTCTCTAGT 2288
|||||

Db 122 CATCTAAAGTCGATGAAATCTCGAAGTCTCTATCCCAAAACAAAGTGTGAATAGTGAT 181
|||||
Qy 2289 CATCTAAAGTCGATGAAATCTCGAAGTCTCTATCCCAAAACAAAGTGTGAATAGTGAT 2348
|||||

Db 182 AATGGAGATGATTAAT 199
|||||
Qy 2349 AATGGAGATGATTAAT 2366
|||||

RESULT 3
LOCUS C39290 360 bp mRNA EST 10-SEP-1997
DEFINITION C39290 Yuji Kohara unpublished cdna Caenorhabditis elegans cdna
clone yk198f10 5', mRNA sequence.
ACCESSION C39290
NID 92375527
VERSION C39290.1 GI:2375527
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
Sano, M., Miyata, A. and Nishigaki, A.
Expression map of the C.elegans genome
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393644.
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykohara@dbj.nig.ac.j.
Location/Qualifiers
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk198f10"
/clone_lib="Yuji Kohara unpublished cdna"

BASE COUNT 102 a 67 c 100 g 91 t

Query Match
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTCTGACTACGGTCAAGATAGAGAGTCAACCATCAGCCGAAGATGATCGCTCAAGATAGA 60
|||||
Qy 2190 CTCTGACTACGGTCAAGATAGAGAGTCAACCATCAGCCGAAGATGATCGCTCAAGATAGA 2249
|||||

Db 61 AGGAGCTTGCTAGAGAGACATTATGATGTTCTCTAGTCAATCTAAAGTCGATGAAAT 120
|||||
Qy 2250 AGGAGCTTGCTAGAGAGACATTATGATGTTCTCTAGTCAATCTAAAGTCGATGAAAT 2309
|||||

Db 121 CTCGAAGTCTCATCGCAACACAGTCTTGAATGATGATTAATGATGATTAAT 177
|||||

Query Match
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 GTCAACCATCAGCCGAAGATGATGCGTCAAGATAGAGAGCTTCTAGAGAGGAACATT 76
|||||
Qy 2214 GTCAACCATCAGCCGAAGATGATGCGTCAAGATAGAGAGCTTCTAGAGAGGAACATT 2273
|||||

Db 77 ATGATGTTCTCTAGTCAATCTAAAGTCGATGAAATTTCTCGAAGTTCATCGCAAAACAA 136
|||||
Qy 2274 ATGATGTTCTCTAGTCAATCTAAAGTCGATGAAATTTCTCGAAGTTCATCGCAAAACAA 2333
|||||

Db 137 GTGTTGAATAGTGAATGAGATGATTAAT 169
|||||
Qy 2334 GTGTTGAATAGTGAATGAGATGATTAAT 2366
|||||

Query Match
Best Local Similarity 100.0%; Pred. No. 1.03e-296;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 GTCAACCATCAGCCGAAGATGATGCGTCAAGATAGAGAGCTTCTAGAGAGGAACATT 76
|||||
Qy 2214 GTCAACCATCAGCCGAAGATGATGCGTCAAGATAGAGAGCTTCTAGAGAGGAACATT 2273
|||||

Db 77 ATGATGTTCTCTAGTCAATCTAAAGTCGATGAAATTTCTCGAAGTTCATCGCAAAACAA 136
|||||
Qy 2274 ATGATGTTCTCTAGTCAATCTAAAGTCGATGAAATTTCTCGAAGTTCATCGCAAAACAA 2333
|||||

Db 137 GTGTTGAATAGTGAATGAGATGATTAAT 169
|||||
Qy 2334 GTGTTGAATAGTGAATGAGATGATTAAT 2366
|||||

RESULT 5
LOCUS C29898 300 bp mRNA EST 09-SEP-1997
DEFINITION C29898 Yuji Kohara unpublished cdna Caenorhabditis elegans cdna
clone yk228a6 3', mRNA sequence.
ACCESSION C29898
NID 92361694
VERSION C29898.1 GI:2361694
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
```

TITLE Sano, M., Miyata, A. and Nishigaki, A.
JOURNAL Expression map of the C.elegans genome
COMMENT Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393504.

Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykohara@dbj.nig.ac.jp.

Location/Qualifiers

1..300
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(el489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue.type=whole animal"
/db_xref="taxon:6239"
/clone="yk228a6"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 111 a 42 c 60 g 86 t 1 others

ORIGIN

Query Match 0.4%; Score 29; DB 15; Length 300;
Best Local Similarity 96.7%; Pred. No. 5.37e-15;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 171 TACTGTANTTTTCGCTACGAGATATTTTC 200

||||| ||||||| ||||||| |||||||

Cp 1423 TACTGTAGTTTCGCTACGAGATATTTTC 1394

RESULT 6

LOCUS D64660 337 bp mRNA EST 13-DEC-1995
DEFINITION CELK086DZR Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk86d12 3', mRNA sequence.

ACCESSION D64660

NID G1116350

VERSION D64660.1 GI:1116350

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 337)
Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
Tabara, H.

Toward an expression map of the C.elegans genome

Unpublished (1994)

On Apr 14, 1993 this sequence version replaced gi:503294.

Contact: Yuji Kohara

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Tel: 0559-75-0771

Fax: 0559-75-6240

Email: ykohara@dbj.nig.ac.jp

High quality sequence stop: 267.

Location/Qualifiers

1..337
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(el489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue.type=whole animal"
/db_xref="taxon:6239"
/map="17"
/clone="yk86d12"

BASE COUNT 116 a 52 c 72 g 94 t 3 others

ORIGIN

Query Match 0.4%; Score 29; DB 32; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.37e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 178 TACTGTAGTTTCGCTACGAGATATTTTC 206

||||| ||||||| ||||||| |||||||

Cp 1423 TACTGTAGTTTCGCTACGAGATATTTTC 1395

RESULT 7

LOCUS T01235 359 bp mRNA EST 10-NOV-1992
DEFINITION wEST01956 Early embryo, Stratagene (cat. #937007) Caenorhabditis
elegans cDNA clone CEES041, mRNA sequence.

ACCESSION T01235

NID 9277716

VERSION T01235.1 GI:277716

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 359)

McCombie, W.R., Kelley, J.M., Aubin, L., Goscochea, M.,
FitzGerald, M.G., Wu, A., Adams, M.D., Dubnick, M., Kerlavage, A.R.,
Venter, J.C. and Fields, C.A.

Caenorhabditis elegans CDNAs

Unpublished (1993)

Other ESTs: wEST01957

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

Seq primer: M13 Forward.

Location/Qualifiers

1..359

/organism="Caenorhabditis elegans"

/db_xref="taxon:6239"

/clone="CEES041"

/clone_lib="Early embryo, Stratagene (cat. #937007)"

BASE COUNT 115 a 61 c 60 g 122 t 1 others

ORIGIN

Query Match 0.4%; Score 31; DB 8; Length 359;

Best Local Similarity 100.0%; Pred. No. 2.09e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 TACAGTAGTCATTAAAGGATTACTGTAGTT 52

||||| ||||||| ||||||| |||||||

QY 1527 TACAGTAGTCATTAAAGGATTACTGTAGTT 1557

RESULT 8

LOCUS C50455 360 bp mRNA EST 11-SEP-1997
DEFINITION C50455 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk483h7 5', mRNA sequence.

ACCESSION C50455

NID 92387708

VERSION C50455.1 GI:2387708

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)

Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
Sano, M., Miyata, A. and Nishigaki, A.

Expression map of the C.elegans genome

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1406982.

Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykohara@dbj.nig.ac.jp.

FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk438h7"
/clone_lib="Yuji Kohara unpublished cDNA"
115 a 60 c 68 g 117 t

BASE COUNT
ORIGIN
Query Match 0.4%; Score 28; DB 15; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.43e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 GTGGCCTTTAAGGAGTACTGTATTTC 126
|||||
Cp 5264 GTGGCCTTTAAGGAGTACTGTATTTC 5237
|||||

RESULT 9
LOCUS D75308 360 bp mRNA EST 14-DEC-1995
DEFINITION CELK098H4F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk98H4 5', mRNA sequence.
ACCESSION D75308
NID g1121092
VERSION D75308.1 GI:1121092
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidae; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
Tabara, H.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1994)
COMMENT

Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykohara@dbj.nig.ac.jp
Insert Length: 895 Std Error: 0.00
High quality sequence stop: 363.

FEATURES
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1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk98H4"
/clone_lib="Yuji Kohara unpublished cDNA"
107 a 81 c 52 g 119 t 1 others

BASE COUNT
ORIGIN
Query Match 0.4%; Score 27; DB 32; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.01e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 GTCAATTAAGAATTAAGTACTGTAGTTTC 115
|||||

Cp 1437 GTCAATTAAGAATTAAGTACTGTAGTTTC 1411

RESULT 10
LOCUS B01439 66 bp DNA GSS 26-JUN-1996
DEFINITION CSRL-131f8-u CSRL flow sorted Chromosome 11 specific cosmid Homo
sapiens genomic clone CSRL-131f8, genomic survey sequence.
ACCESSION B01439
NID g1410717
VERSION B01439.1 GI:1410717
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 66)
AUTHORS Jones, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,
Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S.,
Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M.,
Kupfer, K. and Garner, H.R.
TITLE Genomic Sequence Sampled Map of Chromosome 11
JOURNAL Unpublished (1996)
COMMENT

Contact: Evans CA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
Email: ge Evans@utsw.swmed.edu, shane@mcdermott.swmed.edu
Seg primer: T7
Class: cosmid ends
High quality sequence stop: 66.
Location/Qualifiers
1..66
/organism="Homo sapiens"
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hamster Ovary (CHO) monochromosomal
somatic cell hybrid, J1"
/db_xref="taxon:9606"
/clone="CSRL-131f8"
/clone_lib="CSRL flow sorted Chromosome 11 specific
cosmid"
/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
9 a 4 c 18 g 34 t 1 others

BASE COUNT
ORIGIN
Query Match 0.3%; Score 21; DB 37; Length 66;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 AGATGTGTGTGTGTGTGTG 28
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Cp 2830 AGATGTGTGTGTGTGTG 2810

RESULT 11
LOCUS B36009 96 bp DNA GSS 16-OCT-1997
DEFINITION HS-1031-A2-H07-MR.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate-C7 811 Col-14 Row-O, genomic survey
sequence.
ACCESSION B36009
NID g2535378
VERSION B36009.1 GI:2535378
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 96)
AUTHORS Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,

Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Unpublished (1997)

Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackroneu.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: O column: 14
Class: BAC ends
High quality sequence stop: 96.
Location/Qualifiers

FEATURES

source
1..96
/organism="Homo sapiens"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
/db_xref="taxon:9606"
/clone="Plate-CT 811 Col=14 Row=O"
/clone.lib="CIT Human Genomic Sperm Library C"
/sex="M"

BASE COUNT 16 a 16 c 32 g 32 t
ORIGIN

Query Match 0.3%; Score 21; DB 37; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 TGTGTGTGTGTGTGTGACA 52
|||||
Cp 2827 TGTGTGTGTGTGTGTGACA 2807

RESULT 12
LOCUS AA084532 109 bp mRNA EST 02-FEB-1997
DEFINITION zff6c11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:382868 5', mRNA sequence.
ACCESSION AA084532
NID 91626588
VERSION AA084532.1 GI:16265588
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 109)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfsing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

TITLE WashU-Merck EST Project
JOURNAL
COMMENT On Apr 14, 1993 this sequence version replaced gi:692640.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 291 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.

FEATURES

source
1..109
/organism="Homo sapiens"
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGAGCGCGCGTTTTTTTTTTTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Fatima Bonaldo.
/db_xref="GDB:1291125"
/db_xref="taxon:9606"
/clone="IMAGE:382868"
/clone.lib="Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"

BASE COUNT 33 a 25 c 17 g 33 t
ORIGIN

Query Match 0.3%; Score 20; DB 36; Length 109;
Best Local Similarity 95.2%; Pred. No. 1.19e-01;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 52 GNCACACACACACACACAT 72
|
QY 2808 GTCACACACACACACACAT 2828

RESULT 13
LOCUS AA210472 122 bp mRNA EST 19-FEB-1997
DEFINITION mu30g03.r1 Soares 2NDBT Mus musculus cDNA clone IMAGE:640948 5',
mRNA sequence.
ACCESSION AA210472
NID 91807769
VERSION AA210472.1 GI:1807769
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 122)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geiseli,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1397488.

TITLE The WashU-HHMI Mouse EST Project
JOURNAL
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:392940

Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 105.

FEATURES

source
1..122
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"

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/nap="19"
/clone="IMAGE:640948"
/clone_lib="Soares 2NDMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"

BASE COUNT      29 a      9 c      43 g      41 t
ORIGIN

Query Match      0.3%; Score 22; DB 9; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.90e-04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 GAGATGTGTGTGTGTGTGTG 102
|||||
Cp 2831 GAGATGTGTGTGTGTGTGTG 2810

RESULT 14
LOCUS      AQ308985      126 bp      DNA      GSS      21-DEC-1998
DEFINITION CITBI-E1-2525L8.TF CITBI-E1 Homo sapiens genomic clone 2525L8,
genomic survey sequence.
ACCESSION      AQ308985
NID      94041019
VERSION      AQ308985.1 GI:4041019
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 126)
AUTHORS      Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE      Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL      Unpublished (1998)
COMMENT      Other_GSSs: CITBI-E1-2525L8.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
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1..126
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/sex="male"
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37 a      6 c      48 g      35 t
BASE COUNT
ORIGIN

Query Match      0.3%; Score 21; DB 41; Length 126;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 TGTGTGTGTGTGTGTGTGACA 62
|||||
Cp 2827 TGTGTGTGTGTGTGTGTGACA 2807

/nap="19"
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/clone_lib="Soares 2NDMT"
/sex="male"
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/dev_stage="4 weeks"
/lab_host="DH10B"

BASE COUNT      29 a      9 c      43 g      41 t
ORIGIN

Query Match      0.3%; Score 22; DB 9; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.90e-04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 GAGATGTGTGTGTGTGTGTG 102
|||||
Cp 2831 GAGATGTGTGTGTGTGTGTG 2810

RESULT 14
LOCUS      AQ308985      126 bp      DNA      GSS      21-DEC-1998
DEFINITION CITBI-E1-2525L8.TF CITBI-E1 Homo sapiens genomic clone 2525L8,
genomic survey sequence.
ACCESSION      AQ308985
NID      94041019
VERSION      AQ308985.1 GI:4041019
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 126)
AUTHORS      Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE      Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL      Unpublished (1998)
COMMENT      Other_GSSs: CITBI-E1-2525L8.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
FEATURES
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1..126
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/notes="vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
37 a      6 c      48 g      35 t
BASE COUNT
ORIGIN

Query Match      0.3%; Score 21; DB 41; Length 126;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 TGTGTGTGTGTGTGTGTGACA 62
|||||
Cp 2827 TGTGTGTGTGTGTGTGTGACA 2807

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```

RESULT 15
LOCUS      AA067881      136 bp      mRNA      EST      06-FEB-1997
DEFINITION mm32f03.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:523229 5', mRNA sequence.
ACCESSION      AA067881
NID      g1566161
VERSION      AA067881.1 GI:1566161
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 136)
AUTHORS      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Watson,R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      On Sep 12, 1996 this sequence version replaced gi:1394336.
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG:317077
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 128.
Location/Qualifiers
1..136
/organism="Mus musculus"
/strain="C57BL/6"
/notes="Organ: skin; Vector: pbluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTCCTTTTTCCTTTT 3'"
/db_xref="taxon:10090"
/clone="IMAGE:523229"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"

BASE COUNT      23 a      39 c      24 g      50 t
ORIGIN

Query Match      0.3%; Score 21; DB 35; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 TGTGTGTGTGTGTGTGTGACA 38
|||||
Cp 2827 TGTGTGTGTGTGTGTGTGACA 2807

Search completed: Mon Aug 9 00:23:21 1999
Job time : 12755 secs.

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